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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:02:08 ; Search time 69.1874 Seconds
(without alignments)
235.865 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599
Perfect score: 630
Sequence: 1 PTKLFEPTBECNGYVAGEE.....CPPLHKQGVYANQNGRC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	100.0	696	AA154457	Amino acid sequence
2	630	100.0	696	AAU07190	Human disintegrin
3	630	100.0	696	AB878130	Amino acid sequence
4	630	100.0	832	AA130207	Amino acid sequence
5	630	100.0	832	AA125120	Human MDC3 protein
6	630	100.0	832	AA147778	ADAM 23. Homo sapi
7	630	100.0	832	ABU56479	Lung cancer-associ
8	630	100.0	832	ABU56563	Lung cancer-associ
9	586	93.0	540	AAE13059	ADAM-23dis-Fc fusi

10	404.5	64.2	488	AAE67757	Human fetal brain
11	404.5	64.2	524	AAE67758	Human fetal brain
12	404.5	64.2	16	AAE67759	Human fetal brain
13	404.5	64.2	16	AAE75152	Human fetal brain
14	363.5	57.7	823	AA125119	Human MDC2-beta pr
15	363.5	57.7	859	AA125118	Human MDC2-alpha p
16	363.5	57.7	867	AA130208	Amino acid sequenc
17	338.5	53.7	542	AAE13058	ADAM-22dis-Fc fusi
18	292	46.3	686	AAO14360	Human metalloprote
19	292	46.3	802	AAE67105	First splice varia
20	292	46.3	802	ABE78239	Amino acid sequenc
21	292	46.3	812	ABR00942	Gene 216 alternati
22	292	46.3	812	AAE47106	Second splice vari
23	292	46.3	812	ABE78300	Amino acid sequenc
24	292	46.3	812	AAU98885	Human protease PR
25	292	46.3	812	AAO14377	Human metalloprote
26	292	46.3	812	ABU55870	Human 216 protein
27	292	46.3	813	AAU29256	Human PRO polypept
28	292	46.3	813	ABU71344	Human PRO1891 prot
29	292	46.3	813	ABU65801	Human secreted/tra
30	292	46.3	813	ABU66134	Novel human secret
31	292	46.3	813	ABU67638	Human secreted/tra
32	292	46.3	813	ABU65496	Human PRO polypept
33	292	46.3	813	ABU58632	Human PRO polypept
34	292	46.3	813	ABU56168	Human secreted/tra
35	292	46.3	813	ABU57163	Human PRO polypept
36	292	46.3	813	ABU10742	Human secreted/tra
37	292	46.3	826	ABR00926	Gene 216 polypept
38	292	46.3	826	ABU55849	Human gene 216 pro
39	292	46.3	874	ABU10599	Human novel protei
40	292	46.3	882	AAU72898	Human metalloprote
41	292	46.3	895	ABU10598	Human novel protei
42	292	46.3	914	ABU10597	Human novel protei
43	279	44.3	522	AAE13054	ADAM-15dis-Fc fusi
44	278	44.1	709	AAE98801	CR11-7 nerve prote
45	276.5	43.9	1569	ABE63422	Drosophila melanog

ALIGNMENTS

RESULT 1	
AA154457	
ID	AA154457 standard; Protein: 696 AA.
XX	
AC	AA154457;
XX	
DT	25-APR-2000 (first entry)
XX	
DE	Amino acid sequence of a disintegrin homologue designated zdint1.
XX	
KW	Human, disintegrin homologue; zdint1; cardiac myocyte; adipocyte;
KW	gene therapy; cell-cell interaction; chondro sarcoma; atherosclerosis;
KW	Alzheimer's disease; restenosis; ischemic reperfusion; obesity;
KW	intimal hyperplasia; tumour; platelet aggregation; apoptosis;
KW	neurogenesis; myogenesis; arthritis; myogenesis; neurogenesis;
KW	connective tissue disorder; chondrogenesis; tumour proliferation;
KW	inflammation.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Domain
FT	1..163
FT	/note="propeptide sequence"
FT	164..382
FT	/note="specifically claimed in claim 4"
FT	Domain
FT	383..464
FT	/note="disintegrin sequence; this sequence is
FT	specifically claimed in claim 5"
FT	Misc-difference 437..450
FT	/note="this sequence is specifically claimed in claim 2"
FT	438..449
FT	Region

FT	Region	/note= "disintegrin loop"
FT	443..445	
FT	/note= "RGD binding loop"	
FT	465..696	
FT	Domain	
FT	/note= "cysteine-rich domain; this sequence is specifically claimed in claim 6"	
FT		
PN	WO200002912-A2.	
XX		
XX	20-JAN-2000.	
PD		
XX		
PF	09-JUL-1999;	99WO-US15638.
XX		
PR	10-JUL-1999;	98US-0113883.
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Sheppard PO, Balindur N, Deisher TA, Bishop PD,	
DR	WPI, 2000-160898/14.	
DR	N-P8DB; AAZ45826.	
XX		
PT	Polypeptide useful in modulating cell-cell interaction in tissues of heart, brain, spinal cord and treating chondro sarcoma.	
PT	atherosclerosis, restenosis, obesity, intimal hyperplasia and tumors -	
PS	Claim 7; Page 127-129; 132pp; English.	
XX		
CC	The present sequence represents a human disintegrin homologue, designated	
CC	zdint1. The zdint1 polypeptide is a cardiac myocyte proliferation and	
CC	differentiation stimulator, as well as an adipocyte proliferation and	
CC	differentiation inhibitor. Polynucleotides encoding zdint1 are used in	
CC	gene therapy. The zdint1 polypeptide is useful in modulating cell-cell	
CC	interactions of cells derived from tissues of heart, brain, spinal cord	
CC	and skeletal muscle. It is useful in treating and diagnosing chondro	
CC	sarcoma, atherosclerosis, Alzheimer's disease, restenosis, ischemic	
CC	reperfusion, obesity, intimal hyperplasia and tumors of heart, brain,	
CC	and spinal cord. The zdint1 polypeptide is also useful in identifying	
CC	its new family members, antagonists, agonists and antibodies.	
CC	Antagonists, antibodies and fusion proteins of zdint1 are useful in	
CC	inhibiting platelet aggregation, apoptosis, neurogenesis and myogenesis	
CC	Agonists and antagonists are useful in studying cell-cell interactions,	
CC	arthritis, myogenesis, neurogenesis, connective tissue disorders,	
CC	chondrogenesis, tumour proliferation and suppression, extracellular	
CC	matrix proteins, repair and remodelling of ischemic reperfusion,	
CC	inflammation, and apoptosis.	
XX		
SQ	Sequence 696 AA:	
	Query Match 100.0%; Score 630; DB 21; Length 696;	
	Best Local Similarity 100.0%; Pred. No. 1e-42;	
	Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 PTKLEPPEPCNGGYVAGEECDCGFFVECYGLCKKCSLSNGAHGSDGPCNNNTSCLFQP 60	
Db	373 PTKLEPPEPCNGGYVAGEECDCGFFVECYGLCKKCSLSNGAHGSDGPCNNNTSCLFQP 432	
OY	61 RGEYCRDAVNECDITEYCTGDSGGQCPEPLHKDDGVACNONGRC 104	
Db	433 RGEYCRDAVNECDITEYCTGDSGGQCPEPLHKDDGVACNONGRC 476	
RESULT 2		
ID	AAU07190 standard; Protein; 696 AA.	
XX		
AC	AAU07190;	
XX		
DT	04-DEC-2001 (first entry)	
XX		
DE	Human disintegrin protease, zdint1.	
XX		
KM	Human; disintegrin; zdint1; antiangiogenic; vascular; thrombolytic.	

Key	Location/Qualifiers
Peptide	1..163 /label= Propeptide
Protein	164..696 /label= Mature_zdint1 /note= "This sequence is specifically claimed in claim 4"
Region	164..382 /label= Protease_region /note= "This sequence is specifically claimed in claim 1"
Region	383..464 /label= Disintegrin_sequence /note= "This sequence is specifically claimed in claim 2"
Region	383..696 /label= Disintegrin/cysteine rich sequence /note= "This sequence is specifically claimed in claim 3"
Region	438..449 /label= Disintegrin_loop /label= Disintegrin_loop 443..445 /label= RGD_binding_loop
Binding-site	
US6265199-B1.	
24-JUL-2001.	
09-JUL-1999;	99US-0351414.
10-JUL-1998;	98US-0092371.
(ZYMO) ZYMOGENETICS INC.	
Sheppard PO, Bairdur N, Deisher TA, Bishop PD, Taft DW;	
WPI; 2001-450736/48.	
N-PSDB; AAS11991.	
Disintegrins protease zdint1, useful for producing agents for the development of antithrombotic and anti-migration of tumour cells and have antiangiogenic activity -	
Claim 5; Column 53-56; 50pp; English.	
The invention relates to an isolated novel disintegrin protease family member, zdint1. Disintegrins bind cell surface molecules, including integrins, on the surface of various cells such as platelets, fibroblasts, tumour, endothelial, muscle, neuronal, bone and sperm cells. Disintegrins are unique and potentially useful tools for investigating cell matrix and cell-cell interactions, apoptosis, neurogenesis, connective tissue disorders, chondrogenesis, arthritis, tumour proliferation, ischemia reperfusion and inflammation. Additionally, they are useful in the development of antithrombotic and anti-migration of tumour cells and have antiangiogenic activity. The present sequence represents human disintegrin, zdint1, the gene for which is located on chromosome 2q33.	
Sequence 696 AA;	
Query Match 100.0%; Score 630; DB 22; Length 696;	
Best Local Similarity 100.0%; P-Id. No. 1e-42;	
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Db 373 PTKLFEPTGCGNGVYAGEBDCGFHVECYGLCKKCSLSNGAHCSDGPCNNNTSCLFOP 432
 QY 61 RGYECRDVAVNECDITEYCTGDSGGCCPNNLHKQDGYACNONGRC 104
 433 RGYECRDVAVNECDITEYCTGDSGGCCPNNLHKQDGYACNONGRC 476

RESULT 3
 ABB78130
 ID ABB78130 standard; Protein; 696 AA.
 AC ABB78130;
 DT 05-NOV-2002 (first entry)
 DE Amino acid sequence of human zdin1.
 XX
 KW Human; zdin1; disintegrin protease; platelet accumulation;
 KW chromosome 2q33; platelet aggregation; proteolysis; apoptosis;
 KW neurogenesis; myogenesis; connective tissue disorder; arthritis;
 KW chondrogenesis; cell adhesion; cell fusion; neuron; myocyte; heart;
 KW brain; spinal cord; skeletal muscle tissue; Alzheimer's disease;
 KW tumour formation; multiple sclerosis; congestive heart failure;
 KW ischaemic reperfusion; intimal hyperplasia; restenosis; enzyme.
 KW
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 164..382
 FT Domain /note="protease domain"
 FT 383..464
 FT Domain /note="disintegrin sequence"
 FT 438..449
 FT Region /note="disintegrin loop"
 FT 465..696
 FT Domain /note="cysteine-rich domain"
 FT
 FT
 XX US2002072102-A1.
 XX 13-JUN-2002.
 XX 16-MAR-2001; 2001US-0809790.
 XX
 XX 10-JUL-1998; 98US-092371P.
 XX 09-JUL-1999; 99US-0351414.
 XX
 XX (SHEP/) SHEPPARD P O.
 XX (BAIN/) BAINDOR N.
 XX (DEIS/) DEISHER T A.
 XX (BISH/) BISHOP P D.
 XX
 XX Shepard PO, Bainsdur N, Deisher TA, Bishop PD;
 XX
 XX WPI: 2002-598452/64.
 XX N-PSDB; ABO78447.
 XX
 XX New disintegrin homolog polypeptide and polynucleotide, useful for
 PT modulating cell-cell interactions and diagnosis, treatment of
 PT Alzheimer's disease, tumour formation, multiple sclerosis and congestive
 PT heart failure
 PT
 XX Claim 7; Page 29-30; 53pp; English.
 XX
 XX The present sequence represents a human polypeptide designated zdin1.
 CC zdin1 is a member of the disintegrin protease family. Zdin1 inhibits
 CC platelet accumulation. The zdin1 gene is present on chromosome 2q33.
 CC Zdin1 polypeptides and polynucleotides are useful in treatment of
 CC disorders associated with infarct in brain or heart tissue and/or
 CC platelet aggregation, to modulate proteolysis, apoptosis, neurogenesis,
 CC myogenesis, connective tissue disorders, arthritis, chondrogenesis,
 CC cell adhesion, cell fusion, and signalling or to treat or prevent
 CC development of pathological conditions in such diverse tissue as heart,
 CC brain, spinal cord and skeletal muscle. The molecules modulate

CC inhibition and proliferation of neurons and myocytes in heart, brain,
 CC spinal cord and skeletal muscle tissue. Disorders which may be amenable
 CC to diagnosis, treatment or prevention with zdin1 polypeptides include,
 CC Alzheimer's disease, tumour formation, multiple sclerosis, congestive
 CC heart failure, ischaemic reperfusion or infarct and degenerative
 CC diseases. The zdin1 molecules particularly useful in the treatment of
 CC intimal hyperplasia or restenosis due to acute vascular injury.
 CC
 XX
 SQ Sequence 696 AA;
 Query Match 100.0%; Score 630; DB 23; Length 696;
 Best Local Similarity 100.0%; Pred. No. 1e-42;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PTKLFEPTGCGNGVYAGEBDCGFHVECYGLCKKCSLSNGAHCSDGPCNNNTSCLFOP 60
 373 PTKLFEPTGCGNGVYAGEBDCGFHVECYGLCKKCSLSNGAHCSDGPCNNNTSCLFOP 432
 Db 61 RGYECRDVAVNECDITEYCTGDSGGCCPNNLHKQDGYACNONGRC 104
 433 RGYECRDVAVNECDITEYCTGDSGGCCPNNLHKQDGYACNONGRC 476

RESULT 4
 AAY30207
 ID AAY30207 standard; Protein; 832 AA.
 XX
 XX AAY30207;
 DT 29-OCT-1999 (first entry)
 DE Amino acid sequence of the human SVPH3-17 protein.
 XX
 KW SVPH3-17; metalloproteinase-disintegrin; human chromosome 2;
 KW human chromosome 7; malignant hyperthermia susceptibility;
 KW Zellweger syndrome; neonatal adrenoleukodystrophy;
 KW infantile Refsum disease; progressive familial intrahepatic cholestasis;
 KW mucopolysaccharidosis VII; split hand/foot malformation;
 KW arylphymogenic right ventricular dysplasia-4; Coppock-like cataract;
 KW insulin dependent diabetes mellitus-12; lamellar type ichthyosis;
 KW transient neonatal myaesthesia gravis; congenital aculeiform cataract;
 KW juvenile amyotrophic lateral sclerosis;
 KW familial paroxysmal choreoathetosis;
 KW Finnish lethal neonatal metabolic syndrome.
 KW
 XX Homo sapiens.
 OS
 XX WO9941388-A2.
 XX
 XX 19-AUG-1999.
 XX
 XX 11-FEB-1999; 99WO-US03016.
 XX
 XX 11-FEB-1998; 98US-0074310.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Cerretti DP;
 XX
 XX WPI: 1999-527371/44.
 XX N-PSDB; AA210207.
 XX
 XX DNA encoding the SVPH3-13 and SVPH3-17 proteins for detecting
 PT disease corresponding to chromosome 7, e.g. Zellweger syndrome
 PT
 XX Claim 1; Page 8-9; 82pp; English.
 XX
 XX The present sequence represents a protein designated SVPH3-17, which
 CC is a member of the metalloproteinase-disintegrin family. The
 CC specification also describes SVPH3-13 proteins. Both sequences can
 CC be used to identify human chromosome 2 or 7, and to map genes on these
 CC two chromosomes, and also to identify genes associated with certain
 CC diseases, syndromes, or other human conditions associated with human

CC chromosome 2 or 7. The disease that correspond to chromosome 7 include
 CC malignant hyperthermia susceptibility, Zellweger syndrome, neonatal
 CC adrenoleukodystrophy, infantile Refsum disease, progressive familial
 CC intrahepatic cholestasis, mucopolysaccharidosis VII, and split
 CC hand/foot malformation. Diseases associated with chromosome 2 include
 CC arhythmogenic right ventricular dysplasia-4, insulin dependent diabetes
 CC mellitus-12, transient neonatal myasthenia gravis, juvenile amyotrophic
 CC lateral sclerosis, congenital aequileiform cataract, Copcock-like cataract,
 CC lamellar type ichthyosis, familial paroxysmal choreoathetosis, and
 CC Finnish lethal neonatal metabolic syndrome.

XX Sequence 832 AA;

SO Query Match

Best Local Similarity 100.0%; Score 630; DB 20; Length 832;
 Pred. No. 1.2e-42;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 60

DB 496 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 555

QY 61 RGYECRDVNECDITREYCTGDSGCCPPNLHKODGYACNONGRC 104

DB 556 RGYECRDVNECDITREYCTGDSGCCPPNLHKODGYACNONGRC 599

RESULT 5

AAV25120 standard; Protein; 832 AA.

XX AAV25120;

DT 26-AUG-1999 (first entry)

XX Human MDC3 protein.

KW Metalloproteinase-like-disintegrin-like cysteine rich protein; human;

XX MDC2-alpha; MDC2-beta; MDC3; medical; treatment; diagnosis.

OS Homo sapiens.

PN JP1155574-A.

XX 15-JUN-1999.

PF 01-DEC-1997; 97JP-0330020.

PR 01-DEC-1997; 97JP-0330020.

XX (EISA) EISAI CO LTD.

PA WPI: 1999-398071/34.

DR N-PSDB; AAI78438.

XX New protein belonging to MDC gene family - useful in medical

PT treatment and diagnosis

PS Disclosure: Page 13-16; 17pp; Japanese.

XX This invention describes novel human MDC2-alpha, MDC2-beta and MDC3

CC proteins and their encoding nucleic acids. The products of the invention

CC are useful in medical treatment and diagnosis.

XX Sequence 832 AA;

QY Query Match

Best Local Similarity 100.0%; Score 630; DB 20; Length 832;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 60

DB 496 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 555

QY 61 RGYECRDVNECDITREYCTGDSGCCPPNLHKODGYACNONGRC 104

DB 556 RGYECRDVNECDITREYCTGDSGCCPPNLHKODGYACNONGRC 599

RESULT 6

AAV47778 standard; Protein; 832 AA.

XX AAV47778;

DT 04-MAR-2002 (first entry)

XX ADAM 23.

KW Disintegrin; ADAM 23; metalloproteinase; domain; adhesion; proteolysis;

XX modulator; alpha-v-beta3 integrin; tumour progression; neural tissue;

OS anglogenesis.

XX Homo sapiens.

PN WO200174857-A2.

XX 11-OCT-2001.

PF 02-APR-2001; 2001WO-US10729.

PR 03-APR-2000; 2000US-194164P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA Lopez-Otin C, Freilji JMP, Bianchi AB, Miguel SC, Garcia JML;

PI Trail P;

DR WPI: 2002-066298/09.

XX N-PSDB; AAI72025.

PT Nucleic acid encoding a new ADAM family member, designated ADAM 23 is

PT useful to find modulators of its interaction with integrin which can be

XX used to prevent angiogenesis or increase neural growth -

PS Disclosure: Page 38-41; 44pp; English.

XX This sequence shows a cellular disintegrin, ADAM 23, which is a

CC protein having a disintegrin and metalloproteinase domain. This

CC protein can perform both adhesion and proteolysis functions.

CC Modulators of the interaction between ADAM and alpha-v-beta3 integrin

CC are used to inhibit tumour progression or induce growth of neural

CC tissue. These compounds modulate angiogenesis and growth of matrix

CC metalloproteinases facilitating migration of tumour cells and growth of

XX neural tissue.

XX Sequence 832 AA;

QY Query Match

Best Local Similarity 100.0%; Score 630; DB 23; Length 832;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 60

DB 496 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFOP 555

QY 61 RGYECRDVNECDITREYCTGDSGCCPPNLHKODGYACNONGRC 104

DB 556 RGYECRDVNECDITREYCTGDSGCCPPNLHKODGYACNONGRC 599

RESULT 7

ABU56479

ID ABUS6479 standard; Protein: 832 AA.
XX
AC ABUS6479;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #72.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KM antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN W0200286443-A2.
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US12476.
XX
PR 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI: 2003-093161/08.
DR N-PSDB: ABX76201.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
PS Claim 27; Page 243-244; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
CC polypeptides of the invention.
XX
SQ Sequence 832 AA;
XX
Query Match 100.0%; Score 630; DB 24; Length 832;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PTKLFBPECGNGVAGEECDCGFHVACVGLCKCKKSLNGAHCSDPCCNNTSCLP 60
DB 496 PTKLFBPECGNGVAGEECDCGFHVACVGLCKCKKSLNGAHCSDPCCNNTSCLP 555

OY 61 RGYECRDVANECDITEXCTGDSGCCPPNHLKODGYACNONGRC 104
DB 556 RGYECRDVANECDITEXCTGDSGCCPPNHLKODGYACNONGRC 599
RESULT 8
ID ABUS6563 standard; Protein: 832 AA.
XX
AC ABUS6563;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #156.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KM antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN W0200286443-A2.
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US12476.
XX
PR 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI: 2003-093161/08.
DR N-PSDB: ABX76292.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
PS Claim 27; Page 308; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
CC polypeptides of the invention.
XX
SQ Sequence 832 AA;
XX
Query Match 100.0%; Score 630; DB 24; Length 832;

Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLEPPEPCGGYVAGEBECDCGFHVECYGLCKKCSLSNAGHSDGPPCCNNTSCLFOP 60
DB 466 PTKLEPPEPCGGYVAGEBECDCGFHVECYGLCKKCSLSNAGHSDGPPCCNNTSCLFOP 555

QY 61 RGYECRDVAINECDITEYCTGDSGCCPPNLHKODGYACNONGRC 104
DB 556 RGYECRDVAINECDITEYCTGDSGCCPPNLHKODGYACNONGRC 599

RESULT 9
AAE13059 standard; Protein; 540 AA.
ID AAE13059
XX AAE13059;
AC AAE13059;
XX 28-JAN-2002 (first entry)
DT
XX
DE ADAM-23dis-Fc fusion construct.

Human; ADAM disintegrin domain; integrin; endothelial cell migration;
angiogenesis; ocular disorder; inflammatory disease; bone resorption;
osteoporosis; restenosis; thrombosis; tissue repair; wound healing;
retinopathy; retinoblastoma; neovascular glaucoma; macular degeneration;
retrolental fibroplasia; inflammatory bowel disease; rubecosis; uveitis;
arthritis; rheumatism; myocardial infarction; coronary artery disease;
tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;
preclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;
IgK; Fc region; antiinflammatory; osteopathic; vasolytic; thrombolytic.

OS Chimeric - Homo sapiens.
XX Chimeric - Unidentified.
FH
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= IgK_leader_sequence
FT 21..540
FT /note= "Mature ADAM-23dis-Fc fusion construct"
FT Region 23..310
FT /note= "Human ADAM disintegrin"
FT Domain 34..91
FT /label= Human_ADAM_disintegrin_domain
FT Region 313..540
FT /note= "Fc region"

XX WO200162905-A2.
PN
PD 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US05701.
PF
XX 25-FEB-2000; 2000US-184865P.
PR
XX (IMMUNEX CORP.
PA
PI Fanlow WC, Cerretti DP, Pindexter KM, Black RA;
XX WPI; 2001-625725/72.
DR N-PSDB; AAD21439.
XX
XX Antagonizing the binding of an integrin to its ligand useful for the
PT treatment of angiogenesis comprises administration of an
PT ADAM-disintegrin domain polypeptide -
XX
XX Claim 11; Page 60-61; 66p; English.
XX
XX The invention relates to the method and use of ADAM disintegrin domain
CC polypeptides for inhibiting the biological activity of integrins,
CC endothelial cell migration and angiogenesis. ADAM disintegrin domain
CC polypeptides are used for treatment of ocular disorders, malignant and
CC metastatic conditions, inflammatory diseases, osteoporosis and other

CC conditions mediated by accelerated bone resorption, restenosis,
CC inappropriate platelet activation, recruitment or aggregation, thrombosis
CC or a condition requiring aggregation, thrombosis or a condition requiring
CC tissue repair or wound healing, angiogenesis, ocular neovascularisation
CC or solid tumour, diabetic retinopathy, retinopathy or prematurity,
CC neovascular glaucoma, retinoblastoma, retrolental fibroplasias, rubecosis,
CC uveitis, macular degeneration and corneal graft neovascularisation,
CC inflammatory diseases, ocular tumours, diseases associated with chorioidal
CC or iris neovascularisation, arthritis, rheumatism, inflammatory bowel
CC disease, psoriasis, coronary artery disease or injury, myocardial
CC infarction or injury following myocardial infarction, stroke, unstable
CC angina, atherosclerosis, arteriosclerosis, preclampsia, embolism,
CC platelet-associated ischaemic disorders including lung ischaemia,
CC coronary ischaemia, cerebral ischaemia, restenosis following percutaneous
CC coronary intervention including angioplasty, atherectomy, stent placement
CC and bypass surgery, thrombotic disorders including coronary artery
CC thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis and
CC coagulopathies associated with exposure to a foreign or injured tissue
CC surface and reocclusion following thrombosis, deep venous thrombosis,
CC pulmonary embolism, transient ischaemic attacks and another conditions
CC where vascular occlusion is a common underlying feature, in individuals
CC at high risk for thrombus formation of reformation, advanced coronary
CC artery disease, or for occlusion, reocclusion, stenosis and/or restenosis
CC of blood vessels or stroke benign tumours and preneoplastic conditions,
CC myocardial angiogenesis, haemophilic joints, scleroderma, vascular
CC adhesions, asthma and allergy, eczema and dermatitis, graft versus host
CC disease, sepsis, adult respiratory distress syndrome, telangiectasia and
CC wound granulation. The method are used in combination with angioplasty
CC procedures, such as balloon angioplasty, laser angioplasty, coronary
CC atherectomy or similar techniques, carotid endarterectomy, anastomosis of
CC vascular grafts, surgery having a high risk of thrombus formation (i.e.
CC coronary bypass surgery, stent placement, placement of a chronic
CC and the like), atherectomy, stent placement, placement of a chronic
CC cardiovascular device such as an in-dwelling catheter or prosthetic valve
CC or vessel, organ transplantation or bypass surgery. The present sequence
CC is ADAM disintegrin domain polypeptide fusion construct. The fusion
CC construct comprises of immunoglobulin K (IgK) leader, human ADAM
CC disintegrin and Fc region.

XX SQ Sequence 540 AA;
XX
XX Query Match 93.0%; Score 586; DB 22; Length 540;
XX Best Local Similarity 99.0%; Pred. No. 2.8e-39;
XX Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TECNGYVAGEBECDCGFHVECYGLCKKCSLSNAGHSDGPPCCNNTSCLFOPRGYECRD 67
DB 21 TSCGNGYVAGEBECDCGFHVECYGLCKKCSLSNAGHSDGPPCCNNTSCLFOPRGYECRD 80

QY 68 AVNECDITEYCTGDSGCCPPNLHKODGYACNONGRC 104
DB 81 AVNECDITEYCTGDSGCCPPNLHKODGYACNONGRC 117

RESULT 10
AAR67757
ID AAR67757 standard; Protein; 488 AA.
XX
XX AAR67757;
XX
XX 25-MAR-2003 (updated)
DT 01-AUG-1995 (first entry)
XX
XX Human fetal brain MDC protein.
DE
XX MDC protein; breast cancer; mamma carcinoma; ovary cancer;
KW chromosome-17.
XX
XX Homo sapiens.
OS
XX EP633268-A2.
PN
XX

```

PD 11-JAN-1995.
XX 13-MAY-1994; 94EP-0107487.
XX 14-MAY-1993; 93JP-0136602.
PR 22-SEP-1993; 93JP-0257455.
PR 23-FEB-1994; 94JP-0049904.
PR 12-APR-1994; 94JP-0073328.
XX (CANC-) CANCER INST.
PA (EISA ) EISAI CO LTD.
XX Emi M, Nakamura Y;
PI MPI: 1995-038478/06.
DR N-PSDB; AA076119.
XX
XX Novel MDC protein and DNA encoding it - used to develop prods.
PT for the study, diagnosis and therapy of cancers, partic. breast
PT and ovarian cancer
XX
XX Disclosure; Page 73-74; 123pp; English.
XX
XX A detailed map of human chromosome-17 was constructed to analyze the
CC chromosome in breast and ovarian cancer tissues. 2 Novel cDNAs
CC (given in AA076120-21) were obtained from fetal cerebellum that
CC encoded novel MDC proteins (AAR67758-59, respectively). 5'-RACE and
CC RT-PCR revealed the sequence given in AA076122, encoding the MDC given
CC in AAR75352. Sequences common for these clones are given in AA076119
CC and AAR6757, respectively. A genomic DNA sequence (AA076124) for MDC
CC was obtained from cosmid clone CC117-904.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 488 AA:
Query Match 64.2%; Score 404.5; DB 16; Length 488;
Best Local Similarity 65.4%; Pred. No. 8,8e-25;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2
OY 1 PTKLFEPEECNGNYVEAGEBECDCCGPHVECY--GLCKCKCSISNGAHCSDGPCNNNTSCL 57
Db 332 PUKLIDPECCNGFVEAGEBECDCCGVSOCSPRAGNCCCKKCTLTTHAWGSDGLCCRR--CK 389
OY 58 FOPRGVECRDAVNECDITREYCTGDSGCGCPNINHRODGYACNONOGR 104
Db 390 YEPKRVSCREAVNECDIAETCTGDSGCGCPNINHRODGYCTCHEGR 436

```

Search completed: October 21, 2003, 10:08:27
Job time : 71.9874 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 10:00:20 ; Search time 29.424 Seconds
(without alignments)
339.796 Million call updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630
Sequence: 1 PTKLFEPTECGNGYVGEAGE.....CPNHLKQDGYAQNQNGRC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404.5	64.2	524	2	S38539
2	404.5	64.2	670	2	S15967
3	283	44.9	617	2	S48160
4	274	43.5	814	2	G02390
5	261	41.4	903	2	S60257
6	255	40.5	419	2	A59414
7	255	40.5	571	2	S24789
8	255	40.5	609	2	S55270
9	254.5	40.4	357	2	S23403
10	254.5	40.4	734	2	G02937
11	253.5	40.2	734	2	JC4861
12	252	40.0	616	2	A55796
13	247.5	39.3	655	2	JC7850
14	247.5	39.3	660	2	S71949
15	246	39.0	416	2	A37877
16	243	38.6	216	2	JX0265
17	242.5	38.5	610	2	JC7530
18	240	38.1	789	2	S28259
19	239	37.9	600	2	S28259
20	235	37.3	825	2	S55060
21	235	37.3	905	2	S55059
22	233.5	37.1	736	2	S47645
23	233	37.0	735	2	S47645
24	231	36.7	429	2	A42972
25	230.5	36.6	732	2	JX0266
26	228	36.2	209	2	JX0266
27	227	36.0	419	2	S41607
28	225.5	35.8	952	2	T18900
29	223	35.4	549	2	S48169

30	223	35.4	776	2	S28258	androgen-regulated
31	222	35.2	150	2	S60258	meltrin beta - mou
32	222	35.2	473	2	I49283	ADAM 4 protein pre
33	220.5	35.0	713	2	I65253	disintegrin-like t
34	219.5	34.8	777	2	I48100	ADAM 5 protein pre
35	219	34.8	756	2	S47656	tMDC II protein -
36	217	34.4	1042	2	I26644	hypothetical prote
37	213	33.8	826	2	A60385	monocyte surface a
38	209.5	33.3	823	2	S18968	cytokeratin precurs
39	207	32.9	1239	2	T13809	probable disintegr
40	206.5	32.8	512	2	T37819	probable zinc meta
41	201.5	32.0	544	2	S52477	disintegrin (EC 3.
42	198.5	31.5	491	2	S52920	disintegrin (EC 3.
43	198.5	31.5	748	2	S66129	disintegrin (EC 3.
44	181.5	28.8	83	2	F35982	bitan alpha - puff
45	175.5	27.9	83	2	A34156	bitistatin - puff

ALIGNMENTS

RESULT 1
S38539
disintegrin-like metalloproteinase (EC 3.4.24.-), splice form 1 - human
N/Alternate names: ADAM11; MDC
C/Species: Homo sapiens (man)
C/Date: 07-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 26-May-2000
C/Accession: S38539; I52965
R/Emi, M.; Katagiri, T.; Harada, Y.; Saito, H.; Inazawa, J.; Ito, I.; Kasumi, F.; Nakamu
Nature Genet. 5, 151-157, 1993
A/Title: A novel metalloproteinase/disintegrin-like gene at 17q21.3 is somatically rearran
A/Reference number: S38539; MUID:94073190; PMID:8252040
A/Accession: S38539
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-524 <EMI>
A/Cross-references: GB:D17390; NID:G452188; PIDN:BA04213.1; PID:d1004732; PID:g484255
R/Katagiri, T.; Harada, Y.; Emi, M.; Nakamura, Y.
Cytogenet. Cell Genet. 68, 39-44, 1995
A/Title: Human metalloproteinase/disintegrin-like (MDC) gene: exon-intron organization and
A/Reference number: I52965; MUID:95044425; PMID:7956356
A/Accession: I52965
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 7-225; 'D', 227-524 <KAT>
A/Cross-references: GB:D31872; NID:G505090; PIDN:BA06671.1; PID:d1007243; PID:g836684
C/Comment: For an alternative splice form, see PIR:I65967.
C/Genetics:
A/Genes: GDB:MDC; ADAM11
A/Cross-references: GDB:230267; OMIM:155120
A/Map position: 17q21.3-17q21.3
A/Intons: 28/3; 57/2; 82/3; 105/1; 127/3; 152/3; 176/3; 232/2; 260/3; 291/1; 308/2; 341.
C/Superfamily: disintegrin homology
C/Keywords: alternative splicing; hydrolase; metalloproteinase
F.344-427/Domains: disintegrin homology <DIS>

Query Match 64.2% Score 404.5; DB 2; Length 524;
Best Local Similarity 65.4% Pred. No. 2.3e-25;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

OY 1 PTKLFEPTECGNGYVGEAGECDGCFHYECY---GLCCCKSLSGNAGCSDDPCCNNTSCL 57
DB 339 PTKLDPPECGNGYVGEAGEEDCCSVBSCNAGNCKKCTLTHTDAMCSDDLCCRR--CK 396

OY 58 FQPRGVCRAVNECDITTEYCTGDSGQCPNHLKQDGYACNONGRC 104
DB 397 YEPGVCRAVNECDIAEFTCTGDSGCCPPLHLKLDGYCDHEGRC 443

RESULT 2
I65967
disintegrin-like metalloproteinase (EC 3.4.24.-), splice form 2 - human
N/Alternate names: ADAM11; MDC

C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 17-Mar-2000 #text_change 11-Jan-2002
C:Accession: 165967; S38539
R:Kaagiiri, T.; Harada, Y.; Emi, M.; Nakamura, Y.
R:Kaagiiri, T.; Harada, Y.; Emi, M.; Nakamura, Y.
C:Genet. Cell Genet. 68, 39-44, 1995
A:Title: Human metalloprotease/disintegrin-like (MDC) gene: exon-intron organization and
A:Reference number: 152965; MUID:95044425; PMID:7956356
A:Accession: 165967
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 7-670 <GB>
A:Cross-references: GB:D31872; NID:G505090; PIDN:BA006670.1; PID:G836683
R:Emi, M.; Kaagiiri, T.; Harada, Y.; Satto, H.; Inazawa, J.; Ito, I.; Kasumi, F.; Nakam
Native Genes. 5, 151-157, 1993
A:Title: A novel metalloprotease/disintegrin-like gene at 17q21.3 is somatically rearran
A:Reference number: S38539; MUID:94073190; PMID:8252040
A:Accession: S38539
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225, 'N', 227-495, 'PQGRAWLPLPCLQHLWSSARGGGRQ', <EMI>
A:Cross-references: GB:D17390; NID:G452188; PIDN:BA004213.1; PID:G448255
C:Comment: For an alternative splice form, see PIR:S38539.
C:Genetics:
A:Gene: GDB:MDC; ADAM11
A:Cross-references: GDB:230267; OMIM:155120
A:Map position: 17q21.3-17q21.3
A:Introns: 28/3; 57/2; 82/3; 105/1; 127/3; 152/3; 176/3; 232/2; 260/3; 291/1; 308/2; 341
C:Superfamily: disintegrin homology
C:Keywords: alternative splicing; hydrolase; metalloprotease
C:344-427/Domains: disintegrin homology <DIS>

	Query Match	64.2%	Score 404.5;	DB 2	length 670;	
	Best Local Similarity	65.4%	Pred. No. 2,7e+25;			
	Matches	170;	Conservative	9;	Mismatches 23;	Indels 5; Gaps 2
Oy	1	PTKLEPEPFCGCGYVAGEBECDCGCFHVECY----	GJCCKRCISLNGMHSRSDSGCUNNTSCL	57		
Dd	339	PKLKLDPPBCGCGFPAEBAGECDGASVOESRRAGNCCCKCTILTHDMCSDELCCR--	CK	396		
Oy	58	FQPRGYEGRDAVNECDITLEYCTGDSGCQCPNNHKODGVACNONQGRIC	104			
Dd	397	YEPRVASCRAEVNECDIAETCTGDSGQCPCPNHKDGGVYCTCHDEQGRC	443			

```

RESULT 3
S48160
Metalloproteinase (EC 3.4.24.-) H-I precursor - carpet viper
N:Contains: disintegrin
C:Species: Echis pyramidalis leakeyi
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jul-2000
C:Accession: S48160
R:Paine, M.J.T.; Moura-Da-Silva, A.M.; Theakston, R.D.G.; Crampton, J.M.
Eur. J. Biochem. 224, 483-488, 1994
A:Title: Cloning of metalloproteinase genes in the carpet viper (Echis pyramidalis leakeyi)
A:Reference number: S48160; MUID:95010025; PMID:7925363
A:Accession: S48160
A:Molecule type: mRNA
A:Residues: 1-617 <PBI>
A:Cross-References: GB:X/8970; NID:G763092; PID:CAAS565.1; PID:G763093
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: hydrolase; metalloproteinase; venom
F.1-18/Domain: signal sequence #status predicted <SIG>
F.19-192/Domain: propeptide #status predicted <PRO>
F.193-617/Product: metalloproteinase H-I #status predicted <MAT>
F.403-485/Domain: disintegrin homology <DIS>
F.337/Active site: Glu #status predicted

```

```

Query Match      44.9%  Score 283;  DB 2;  Length 617;
Best Local Similarity 44.8%  Pred. No. 1.2e-15;
Matches 47;  Conservative 17;  Mismatches 37;  Indels 4;  Gaps 2
OY      2  TKLPEPTCGNAYVAGEBCDGFVHECYGLCK--KCLSLNGAHSDDPCCNNNSCLFQ 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 399 TDIIVSVSGVGNFVVEGEECCDGSNTYCRNPCCNATTCKLIRGQCADGECCN--QCRFR 456

Qy 60 PRGEYCRDAVNECDITEYCTGDSGCCPPNLHKQDSYACNQNQGRG 104

Db 457 PARETECRKIDDDVPEYCTGSGSCPLDIVGRNQIPVQSNNGVC 501

```

RESULT 4
G02390
disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1995 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
C:Accession: G02390; P04263
R:Heiren, B.; Raines, E.W.; Ross, R.
Submitted to the EMBL Data Library, January 1996
Reference number: H01157

```

A:Status: preliminary; translated from GB/EMBL/DDbJ
A:Molecule type: mRNA
A:Residues: 1-814 <HER>
A:Cross-references: EMBL:U46005; NID:g1335871; PIDD:AAC5112.1; PID:g1335872
R:McLite, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell, B.
Biochem. Biophys. Res. Commun. 230, 335-339, 1997
A:Title: Expression of members of a novel membrane linked metalloproteinase family (ADMM)
A:Reference number: PC4263; MUID:97168971; PMID:9016778
A:Accession: PC4263
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-461 <MCK>
A:Experimental source: articular chondrocyte
A:Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m
C:Superfamily: mouse metrin alpha; disintegrin homology
C:Keywords: hydrolase; metalloproteinase; zinc
E:430-503/Domain: disintegrin homology <DIS>
E:348,352,358/Binding site: zinc (His) #status predicted
E:349/Active site: Glu #status predicted

Query Match	43.5%	Score 274;	DB 2;	Length 814;
Best Local Similarity	48.5%;	Pred. No. 7.7e-15;		
Matches	50;	Conservative	11;	Mismatches 32;
			Indels	10;
			Gaps	4

QY 10 CGGGYEAEEEDCCGHHVYGLCKCK--CSLSNDAH-SGPGPCNNTSCLFOPRGYECR 66
Db 424 CGGMFFPBBQDCGFLDDCVDPCCDSLTQLRPAQASGAPCCQN--COLRSGMCR 481
QY 67 DAVNECDITTEYCTGDSGCCPEMLAKQDGYACNNQ-----GRC 104
Db 482 PTRGDCDLRPFPGDSSQCPDPVLSAGDEPACGAGGAVCMHRC 524

RESULT 5
S60257
meltrin alpha - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #next_change 20-Jun-2000
C/Accession: S60257
R/Ygam-Hitomasa T.; Sato. T.; Kurisaki, T.; Kamiyo, K.; Nabeshima, Y.I.; Fujisawa-Sen
Nature 377, 652-656, 1995
A/Title: A metalloproteinase-disintegrin participating in myoblast fusion.
A/Reference number: S60257; MUID:96026308; PMID:7566181
A/Accession: S60257
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-903 <YNG>
A/Cross-references: EMBL:DS0411; NID:g1054586; PIRN:BA08912.1; PIR:g1054587
C/Superfamily: mouse meltrin alpha; disintegrin homology
F/421-503/Domain: disintegrin homology <DIS>
F/349/Active site: Glu #status predicted

Query Match	41.4%;	Score 261;	DB 2;	Length 903;
Best Local Similarity	45.1%;	Pred. No. 9e-14;		
Matches 46;	Conservative 12;	Mismatches 40;	Indels 4;	Gaps 2

Qy 5 FEPEECNGVYVGAEECDCCGFHYECYGLCKC --KCSISNGAHSDGHCNNNTSCLFQPG 62
Db 420 FGGRKCGNGVYBSEBEECDCCGPEECTRCCNATTTCTLKPDVCAHGHQCEED --QLKPPG 47
Qy 63 YECGDVAIVEDITFYCTGDSGQCPRYLHKDGYACANQGRIC 104
Db 478 TACRGSSNSCDLPFCCTGTAPHCPCANNYYLHDGHPQGVDDYC 519

RESULT 6

metalloproteinase (EC 3.4.24.-) (brevilysin) H6, venom - *Gloydius halys brevicandus*
 N:Contains: disintegrin
 C:Species: *Gloydius halys brevicandus*
 C:Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 21-Apr-2003
 C:Accession: A59414
 J:Terada, S.
 J:Biochem. 128, 167-173, 2000
 A:Title: Primary Structure and Autoproteolysis of Brevilysin H6 from the Venom of *Gloydius*
 A:Reference number: A59414
 A:Accession: A59414
 A:Status: preliminary
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-419 <TR>
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; venom; zinc
 F:1/Modified site: pyroglutamic acid (Gln) #status experimental
 F:118-198,182-187/D:Disulfide bonds: #status experimental
 F:158-165/D:Disulfide bonds: (or 158-160) #status experimental
 F:181/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match	40.5%	Score 255	DB 2	Length 419
Best Local Similarity	41.9%	Pred.No. 1.7e-13		
Matches 44	Conservative 13	Mismatches 44	Indels 4	Gaps 2

Qy 2 TXLEPPEPGNGVVEAGEEDCGSFHVEGGLCC - KKSLSNGAGCSGPPCNTTSLCFQ 59
Db 206 TDIVSPVVCNELLVEGBECDCGTPEPNCNCECCDAATCKLXGSGQCGDDCCB - QCKFS 265
Qy 60 PRGTECDVAVNECDITTEYCTGDSGQCPNLLHKQDGYACNONGRC 104
Db 264 KSGTECHRESMPEDCPAHECTQSSSECPAVFHNKQGPCPLDNYGVC 308

RESULT 7

J:Jararhagin C precursor - jararaca (fragment)
 N:Alternate names: single chain botrocetin
 N:Contains: disintegrin-like 28k protein; hemorrhagic proteinase (EC 3.4.24.-)
 C:Species: Bothrops jararaca (jararaca)
 C:Date: 20-Feb-1995 #sequence revision 29-Aug-1997 #text_change 09-Jun-2000
 C:Accession: S24789, J02245, A44463, A37958, J02373
 R:Paine, M.J.1.
 submitted to the EMBL Data Library, August 1992
 A:Reference number: S24789
 A:Accession: S24789
 A:Molecule type: mRNA
 A:Residues: 1-571 <PAT>
 A:Cross-references: EMBL:X68251, NID:G62467, PID:G62468
 U:Usami, Y.; Fujimura, Y.; Mitsu, S.; Shima, H.; Yoshida, E.; Yoshioka, A.; Hirano, K.;
 Biochem. Biophys. Res. Commun. 201, 331-339, 1994
 A:Title: A 28 kDa-protein with disintegrin-like structure (jararhagin-C) purified from E
 A:Reference number: J02245, MUID:94256999, PMID:8198592
 A:Accession: J02245
 A:Molecule type: cDNA
 A:Residues: 360-571 <USA>
 A:Experimental source: Venom
 R:Paine, M.J.; Desmond, H.P.; Theakston, R.D.; Crampton, J.M.
 J. Biol. Chem. 267, 22869-22876, 1992
 A:Title: Purification, cloning, and molecular characterization of a high molecular weight
 Jly.
 A:Reference number: A44463, MUID:93054601, PMID:1385408
 A:Accession: A44463
 A:Molecule type: mRNA

A;Residues: 1-23, 'Q', 25-92, 'G', 94-131, 'G', 133-169, 'Q', 171-571 <PA2>
A;Cross-references: GB:X68251

A; Experimental source: venom gland
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBI:P:118104)
R; Fujimura, Y.; Tlani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug
Biochemistry 30, 1957-1964, 1991

A;Reference number: A37958; MUID:91129280; PMID:1993206
A;Accession: A37958

A;Residues: 360-372, 'E', 374-378, 'X', 380-384 <FUJ>
A;Note: 361-Val was also found

C;Comment: Inhibits collagen- and ADP-induced platelet aggregation
C;Superfamily: mouse meltrin alpha; disintegrin homology

C;keywords: hydrolase; metalloproteinase; venom; zinc
F;360-571/Product: jararagin C #status experimental <MAT>
F;362-444/Domain: disintegrin homology <DIS>

F;295,299,305/Binding site: zinc (His) #status predicted
F;296/Active site: Glu #status predicted

Query Match	40.5%	Score 255;	DB 2;	Length 571;
Best Local Similarity	41.9%	Pred. No. 2e-13;		
Matches 44;	Conservative 13;	Mismatches 44;	Indels 4;	Gaps 2;

Qy 2 TKLEPTGNGYVAGEECDGCFVHCYGLCC--KKCSLSNGAHSDGPPCENNTSCLFQ 59
| : ||| : ||||| : : |||
Db 358 TDISPPVCGNELLEVGEEDCGTPENCQNBCCDAATCKLKSQSGHGDCCE--QCKFS 415

```

Oy      60  PRGYECRDVANECDITEYCTGTGDSGCPPNLHKQDGYACNQGRC 104
          | | | | | | | | | | | | | | | | | | | | | |
Db      416  KSGTECRASMSECDPAEHCTGQSSECPADVFHKNQQPCLDNYYYC 460

```

RESULT 8

catrocollastatin precursor - western diamondback rattlesnake
 C|Species: Crocalus atrox (western diamondback rattlesnake)
 C|Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
 C|Accession: S55270
 R|Zhou, Q.; Smith, J.B.; Grossman, M.H.
 Biochem. J. 307, 411-417, 1995
 A|Title: Molecular cloning and expression of catrocollastatin, a snake-venom protein from
 A|Reference number: S55264; MUID:95251603; PMID:7733877
 A|Accession: S55270
 A|Status: Preliminary
 A|Molecule type: mRNA
 A|Residues: 1-609 <ZHO-
 A|Cross-references: GB:U01003; NID:g710353; PION:AACS6672.1; PID:g710354
 C|Superfamily: mouse melittin alpha; disintegrin homology

Query Match	40.5%;	Score 255;	DB 2;	Length 609;
Best Local Similarity	41.9%;	Pred. No. 2.1e-13;		
Matches 44;	Conservative 13;	Mismatches 44;	Indels 4;	Gaps 2;

QY 2 TKLEPTECGNGYVAGEECDCGFFHYECYGLCC--KKCSLSNGAHCSDGPPCCNNTSLCFQ 59
| : | | | : | | | | : | | | |
Db 396 TDIISPPVCGNELLEVGEEDCGTPENCQNECCDAATCKLKSQSGQGCHGDCE--QCKFS 453

Qy 60 PRGYECRDVNECDITEYCTGSDSGCCPNLHKQDGYACNONGRC 104
| | | : : | | : : | : : : | |
Db 454 KSGTECRASWSECDPAEHCTGQSSECPADVFKHNGPCLDNVGYC 498

RESULT 5

sperm surface protein PH-20 beta chain precursor - guinea pig (fragment)
C.Species: *Cavia porcellus* (guinea pig)
C.Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jun-2000
C.Accession: S23403: 625656
R.Ibidell, C.P.; Wolfberg, T.G.; Turck, C.W.; Myles, D.G.; Primakoff, P.; White, J.M.
Nature 356, 248-252, 1992
Article: A potential fusion peptide and an integrin ligand domain in a protein active in

A:Reference number: S23402; MUID:92204234; PMID:1552944

A:Accession: S23403

A:Molecule type: mRNA

A:Residues: 1-357 <BL01>

A:Cross-references: EMBL:Z11720

A:Accession: S23696

A:Molecule type: protein

A:Residues: 5-8,'X',10-32,67-88,125-129,'X',131-134,'X',136-141,'X',143,154,'X',156-161;

C:Superfamily: mouse meltrin alpha; disintegrin homology

C:Keywords: glycoprotein; transmembrane protein

F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>

F:5-357/Product: sperm surface protein PH-30 beta chain #status experimental <MAT>

F:303-323/Domain: disintegrin homology <DIS>

F:78,186,256/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match

40.4%; Score 254.5; DB 2; Length 357;

Best Local Similarity 43.1%; Pred. No. 1,6e-13;

Matches 44; Conservative 15; Mismatches 34; Indels 9; Gaps 3;

OY 10 CGNGVAGEECDCGFHVECYGLCC--KKCSLSNGACSDGPCNNNTSCLFQPRGYECRD 67

DB 9 CGNNVVEGCEDDCCSQEGECODTCCDATCRUKTSRCAQSPCCN--QCEFTKGEVCRE 66

OY 68 AVNECDITEYCTGDSGQCPNLLHKQGYACNQNQ----GRC 104

DB 67 STDECDLPEYCNSSGACQEDLYVINGHRCANEWICMNGRC 108

RESULT 10

G02937

fertilin beta - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 01-Dec-2000

C:Accession: G02937; S55061

R:Ramato, C.S.; Wyles, D.G.; White, J.M.; Primakoff, P.

submitted to the EMBL Data Library, August 1995

A:Reference number: G12615

A:Accession: G02937

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-735 <RAM>

A:Cross-references: EMBL:U33959; NID:9998339; PID:9998340

R:Perly, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.

Biochem. J. 307, 843-850, 1995

A:Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.

A:Reference number: S55059; MUID:9526013; PMID:7741716

A:Accession: S55061

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-722,'S',724-735 <PER>

A:Cross-references: EMBL:X77653; NID:9794076; PIDN:CA54733.1; PID:9794077

C:Superfamily: mouse meltrin alpha; disintegrin homology

F:383-468/Domain: disintegrin homology <DIS>

Query Match

40.4%; Score 254.5; DB 2; Length 735;

Best Local Similarity 46.0%; Pred. No. 2,6e-13;

Matches 46; Conservative 11; Mismatches 36; Indels 7; Gaps 3;

OY 10 CGNGVAGEECDCGFHVECYGL---CC--KKCSLSNGACSDGPCNNNTSCLFQPRGYE 64

DB 387 CGNAKLEAGEECDCGTOQCFLGAKCCDTATCRFAGSNCAGPCCEN--CLFMSQERV 444

OY 65 CRDAVNECDITEYCTGDSGQCPNLLHKQGYACNQNQRC 104

DB 445 CRPSFDECDLPEYCNSTASCPENHFIQTGHPCGPNQWVC 484

Search completed: October 21, 2003, 10:11:33
Job time : 30.434 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:02:08 ; Search time 18.3145 Seconds
(without alignments)
267.045 Million call updates/sec

Title: US-09-634-252A-4_COPY_496_599
Perfect score: 630
Sequence: 1 PTKLFPEPTCGNGYVEAGEE.....CPNLFHKQDGYAQNQNGRC 104

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404.5	64.2	769	AD11_HUMAN	Q75078 homo sapien
2	404.5	64.2	773	AD11_MOUSE	Q911v4 mus musculu
3	375	59.5	452	AD11_XENLA	Q95e23 xenopus lae
4	364.5	57.9	857	AD22_MOUSE	Q911v6 mus musculu
5	363.5	57.7	906	AD22_HUMAN	Q950k1 homo sapien
6	357.5	56.7	935	AD22_XENLA	Q42596 xenopus lae
7	292	46.3	813	AD33_HUMAN	Q95211 homo sapien
8	278	44.1	816	AD15_RAT	Q94Y70 r adam 15 p
9	274	43.5	814	AD15_HUMAN	Q13444 homo sapien
10	269	42.7	797	AD33_MOUSE	Q933w9 mus musculu
11	268	42.5	920	AD19_MOUSE	Q35674 mus musculu
12	267.5	42.5	790	AD30_HUMAN	Q94kf2 homo sapien
13	263	41.7	815	AD15_MOUSE	Q85839 mus musculu
14	262	41.6	909	AD12_HUMAN	Q43134 homo sapien
15	261	41.4	903	AD12_MOUSE	Q61824 mus musculu
16	259.5	41.2	751	AD02_RABIT	Q28650 oryctolagus
17	258	41.0	776	AD28_MACRA	Q95s16 macaca fasc
18	257	40.8	956	AD19_HUMAN	Q95013 homo sapien
19	255	40.5	571	DISJ_BOTJA	P30431 botchops ja
20	254.5	40.4	735	AD02_CAVDO	Q63411 cavia porce
21	254.5	40.4	735	AD02_MACFA	Q28478 macaca fasc
22	254.5	40.4	745	AD02_BOVIN	Q77730 bos taurus
23	253.5	40.2	735	AD02_HUMAN	Q95955 homo sapien
24	252	40.0	616	ECAR_ECHCA	Q90435 echis carin
25	248	39.4	761	AD04_MOUSE	Q91143 mus musculu
26	247.5	39.3	819	AD09_HUMAN	Q13443 homo sapien
27	247	39.2	775	AD28_HUMAN	Q94k52 homo sapien
28	246	39.0	416	HRIB_TRIFL	P20152 trimeresuru
29	244.5	38.8	820	AD29_HUMAN	Q94k65 homo sapien
30	244	38.7	726	AD20_HUMAN	Q43506 homo sapien
31	242	38.4	722	AD21_HUMAN	Q94k18 homo sapien
32	240	38.1	789	AD07_RAT	Q63130 rattus norv
33	235	37.3	788	AD07_MOUSE	Q35327 mus musculu

34	233.5	37.1	697	AD26_MOUSE	Q9158 mus musculu
35	232	36.8	719	AD18_MOUSE	Q9157 mus musculu
36	230	36.5	445	AD18_RAT	P97776 rattus norv
37	223	35.4	754	AD07_HUMAN	Q9h2u9 homo sapien
38	223	35.4	776	AD07_MACFA	Q28475 macaca fasc
39	221.5	35.2	760	AD25_MOUSE	Q9159 mus musculu
40	220	34.9	729	AD18_MOUSE	Q91176 mus musculu
41	218.5	34.7	746	AD18_MACFA	Q95194 macaca fasc
42	217.5	34.5	737	AD02_RAT	Q63202 rattus norv
43	214.5	34.0	739	AD18_HUMAN	Q943q7 homo sapien
44	213	33.8	826	AD08_MOUSE	Q05910 mus musculu
45	211.5	33.6	824	AD08_HUMAN	P78325 homo sapien

ALIGNMENTS

RESULT 1

ID	AD11_HUMAN	STANDARD:	PRT:	769 AA.
AC	Q75078: Q14808; Q14809; Q14810;			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	ADAM 11 precursor (A disintegrin and metalloproteinase domain 11)			
DE	(Metalloproteinase-like, disintegrin-like, and cysteine-rich protein)			
DE	(MDC)			
GN	ADAM11 OR MDC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG).			
RC	TISSUE=Brain;			
RA	MEDLINE=96359734; PubMed=9693107;			
RX	Sagane K., Ohya Y., Hasegawa Y., Tanaka I.;			
RT	"Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2 and MDC3: novel human cellular disintegrins highly expressed in the brain.";			
RL	Biochem. J. 334:93-98(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RC	TISSUE=Brain, Breast, Ovary, and Testis;			
RA	MEDLINE=95044425; PubMed=7956356;			
RX	Katagiri T., Harada Y., Eml M., Nakamura Y.;			
RT	"A novel metalloproteinase/disintegrin-like gene at 17q21.3 is somatically rearranged in two primary breast cancers.";			
RL	Nat. Genet. 5:151-157(1993).			
RN	[3]			
RP	SEQUENCE OF 106-769 FROM N.A. (ISOFORMS LONG AND SHORT).			
RC	TISSUE=Brain, Breast, Ovary, and Testis;			
RA	MEDLINE=95044425; PubMed=7956356;			
RX	Katagiri T., Harada Y., Eml M., Nakamura Y.;			
RT	"Human metalloproteinase/disintegrin-like (MDC) gene: exon-intron organization and alternative splicing.";			
RL	Cytogenet. Cell Genet. 68:39-44(1995).			
CC	- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON CATALYTIC METALLOPROTEINASE-LIKE PROTEIN.			
CC	- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=Long; Synonyms=MDC-769;			
CC	Isoid=075078-1; Sequence=Displayed;			
CC	Name=Short; Synonyms=MDC-524;			
CC	Isoid=075078-2; Sequence=VSP_005472; VSP_005473; VSP_005474, VSP_005475;			
CC	- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN. SLIGHTLY DETECTED OR NOT AT ALL IN OTHER TISSUES.			
CC	- DOMAIN: A CONSERVED MOTIF [AVN(E/D)CD] WITHIN THE DISINTEGRIN-LIKE DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTEGRIN RECEPTOR.			
CC	- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY			

CC SIMILARITY).

CC -1- DISEASE: REARRANGEMENTS OCCUR IN BREAST AND OVARIAN CANCERS WHICH INVOLVE MULTIPLE EXONS AND DISRUPT THE CODING REGION.

CC -1- SIMILARITY: Belongs to peptidase family M12B.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -1- SIMILARITY: Contains 1 disintegrin domain.

CC -----

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CC -----

CC EMBL, AB009675; BAA33352.1; -

CC EMBL, D17390; BAA04213.1; -

CC EMBL, D31872; BAA06670.1; -

CC PIR, I65967; I65967.

CC HSSP, P18619; 1FVL.

CC MEROPS, M12_976; -

CC Genew, HGNC:189; ADAM11.

CC MIM, 155120; -

CC GO, GO:0005886; C:plasma membrane; TAS.

CC GO, GO:0005178; F:integrin binding activity; TAS.

CC GO, GO:0001229; P:integrin-mediated signaling pathway; TAS.

CC InterPro: IPR006586; ADAM cysteine.

CC InterPro: IPR001762; Disintegrin.

CC InterPro: IPR006209; EGF-like.

CC InterPro: IPR002870; Pep_M12B_propep.

CC InterPro: IPR001590; RepPolysin.

CC InterPro: IPR006025; Zn_MTPeptidse.

CC Pfam, PF00200; disintegrin; 1.

CC Pfam, PF01562; Pep_M12B_propep; 1.

CC PRINTS, PR01421; RepPolysin; 1.

CC PRINTS, PR00289; DISINTEGRIN.

CC Prodom, PD000664; Disintegrin; 1.

CC SMART, SM00608; ACR; 1.

CC SMART, SM00050; DISIN; 1.

CC PROSITE, PSS0215; ADAM_MEROP; 1.

CC PROSITE, PSS0427; DISINTEGRIN_1; FALSE_NEG.

CC PROSITE, PSS0214; DISINTEGRIN_2; 1.

CC PROSITE, PSS0022; EGF_1; 1.

CC PROSITE, PSS0186; EGF_2; FALSE_NEG.

CC PROSITE, PSS0142; ZINC_PROTEASE; FALSE_NEG.

CC Signal, Glycoprotein; Transmembrane; EGF-like domain;

CC Alternative splicing.

CC KX SIGNAL 1 23

CC FT PROPEP 24 225

CC FT CHAIN 226 769

CC FT DOMAIN 226 734

CC FT TRANSMEM 735 755

CC FT DOMAIN 756 769

CC FT DOMAIN 226 438

CC FT DOMAIN 444 531

CC FT DOMAIN 532 676

CC FT DOMAIN 677 709

CC FT DISULFID 349 433

CC FT DISULFID 503 516

CC FT DISULFID 677 692

CC FT DISULFID 686 698

CC FT DISULFID 700 709

CC FT CARBOHYD 96 .96

CC FT CARBOHYD 163 163

CC FT CARBOHYD 603 603

CC FT CARBOHYD 673 673

CC FT VARSPLIC 1 99

CC FT VARSPLIC 100 104

CC FT VARSPLIC 595 623

CC FT VARSPLIC 595 623

FT FT VARSPLIC 624 769 /FTid=VSP_005474.

FT FT VARSPLIC 106 106 Missing (in isoform Short).

FT FT CONFLICT 325 325 Q -> H (IN REF. 1).

FT FT CONFLICT 325 325 D -> N (IN REF. 2).

CC SQ SEQUENCE 769 AA; 83409 MW; 5989C4676BDDB66 CRC64;

Query Match 64.2%; Score 404.5; DB 1; Length 769;

Best Local Similarity 65.4%; Pred. No. 4.7e-27;

Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

QY 1 PTKLEPTECGNGVAGEECDCGFHYECY---GLCKKCSLSNGAHCSGSPCCNNTSCL 57

DB 438 PLKLLDPCECGNGVAGEECDCGSGVCECSRAGNCKCKTTLTHAMCSDSGLCCRR--CK 495

QY 58 FOPRGYERDAVNECDITFYCTGSGGCGCPPLHLKODGYACNONGRC 104

DB 496 YEPRGVSCRAVNECDIETCTGDSGCPPLHLKIDGYCDHEGRC 542

RESULT 2

ID AD11_MOUSE STANDARD: PRT: 773 AA.

AC Q9RIV4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE ADAM 11 precursor (A disintegrin and metalloproteinase domain 11)

DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein)

DE (MDC).

GN ADAM11 OR MDC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RC MEDLINE=99365303; PubMed=10433968;

RA Sagane K., Yamazaki K., Mizui Y., Tanaka I.;

RT "Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23.";

RL Gene 236:79-86(1999).

CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON CATALYTIC METALLOPROTEASE-LIKE PROTEIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE BRAIN. WEAKLY DETECTED IN THE HEART, LIVER AND TESTIS.

CC -1- DOMAIN: A CONSERVED MOTIF (AVN(E/D)CD) WITHIN THE DISINTEGRIN-LIKE DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTEGRIN RECEPTOR.

CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY SIMILARITY).

CC -1- SIMILARITY: Belongs to peptidase family M12B.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -1- SIMILARITY: Contains 1 disintegrin domain.

CC -----

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CC -----

CC EMBL, AB009675; BAA83384.1; -

CC HSSP, P18619; 1FVL.

CC MEROPS, M12_976; -

CC MGD, MGI:1098667; Adam11.

CC InterPro: IPR006586; ADAM cysteine.

CC InterPro: IPR001762; Disintegrin.

CC InterPro: IPR006209; EGF-like.

CC InterPro: IPR002870; Pep_M12B_propep.

CC InterPro: IPR001590; RepPolysin.

CC InterPro: IPR006025; Zn_MTPeptidse.

DR Pfam: PF00200; disintegrin. 1.
DR Pfam: PF01562; Rep_M12B_propep. 1.
DR Pfam: PF01421; Repolysin. 1.
DR PRINTS: PR00289; DISINTEGRIN.
DR Pfam: PF000664; disintegrin. 1.
DR SMART: SM00050; ACR. 1.
DR SMART: SM00050; DISIN. 1.
DR PROSITE: PS50215; ADAM_MERO. 1.
DR PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; FALSE_NEG.
DR PROSITE: PS00142; ZINC_PROTEASE; FALSE_NEG.
KW Signal; Glycoprotein; Transmembrane; EGF-like domain.
FT SIGNAL 1 24
FT PROPEP 25 229 BY SIMILARITY.
FT CHAIN 230 773 ADAM 11.
FT DOMAIN 230 738 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 739 759 POTENTIAL.
FT DOMAIN 760 773 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 230 442 METALLOPROTEASE-LIKE.
FT DOMAIN 448 535 DISINTEGRIN-LIKE.
FT DOMAIN 536 680 CYS-RICH.
FT DOMAIN 681 713 EGF-LIKE.
FT DISULFID 353 437 BY SIMILARITY.
FT DISULFID 507 520 POTENTIAL.
FT DISULFID 681 696 BY SIMILARITY.
FT DISULFID 690 702 BY SIMILARITY.
FT DISULFID 704 713 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 677 677 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 773 AA; 84134 MW; 9AB8125FB3F743DD CRC64;

Query Match 64.2%; Score 404.5; DB 1; Length 773;
Best Local Similarity 65.4%; Pred. No. 4.7e-27;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 1 PTKLFEPECGNGVGEAGEGDCGCFHVC---GLCKCKSLNSGAGSDGPCNNNTSC 57
Db 442 PLKLLDPSCGNGFVEAGEEBCDCGSGVOCSPRAGCKCKCTLTMDAMCSDGLCCR--CK 499
Qy 58 FQPRGYECRDVAVECDITEYCTGDSGQCPNHLKOGVACNONGRC 104
Db 500 YEPGVSCEAVNECDIAETCTGDSGQCPNHLKIDGYCHQGR 546

RESULT 3
AD11_XENLA STANDARD; PRT; 452 AA.
AC OPR523;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADAM 11 (A disintegrin and metalloproteinase domain 11)
DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein)
DE (MDC) (Metalloproteinase-disintegrin MDC11a) (MDC11.1) (Fragment).
GN ADAM11 OR MDC11A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
NCBI_Taxid=8355;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RL MEDLINE=99102794; PubMed=9882486;
RA Cal H., Kraetzschmar J., Alfandari D., Hunnicutt G., Blobel C.P.;
RT "Neural crest-specific and general expression of distinct
metallopeptidase-disintegrins in early Xenopus laevis development";
RL Dev. Biol. 204:508-524(1998).
-!- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON

CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: DETECTED IN TESTIS AND BARELY EXPRESSED IN
CC HEART AND MUSCLE. NOT DETECTABLE IN LIVER.
CC -!- DEVELOPMENTAL STAGE: COULD NOT BE DETECTED IN EMBRYOS UNTIL
CC NEURULATION. IN DEVELOPING EMBRYOS, THE EXPRESSION IS RESTRICTED
CC TO NEURAL CREST DERIVATIVES.
CC -!- DOMAIN: A CONSERVED MOTIF (AVN(E/D)CD) WITHIN THE DISINTEGRIN-LIKE
CC DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTEGRIN RECEPTOR.
CC -!- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL: AF032384; AAC61848.1; -!
DR HSSP: P18619; 1FV.
DR MEROPS: M12. UNB. -!
DR InterPro: IPR006586; ADAM cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001590; Repolysin.
DR InterPro: IPR006025; Zn MTpeptidase.
DR Pfam: PF00200; disintegrin. 1.
DR Pfam: PF01421; Repolysin. 1.
DR PRINTS: PR00289; DISINTEGRIN.
DR Pfam: PF000664; disintegrin. 1.
DR SMART: SM00050; ACR. 1.
DR SMART: SM00050; DISIN. 1.
DR SMART: SM00181; EGF. 1.
DR PROSITE: PS50215; ADAM_MERO. 1.
DR PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; FALSE_NEG.
DR PROSITE: PS00142; ZINC_PROTEASE; FALSE_NEG.
KW Glycoprotein; Transmembrane; EGF-like domain.
FT NON_TER 1 1
FT DOMAIN <1 417 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 418 438 POTENTIAL.
FT DOMAIN 439 452 CYTOPLASMIC (POTENTIAL).
FT DOMAIN <1 120 METALLOPROTEASE-LIKE.
FT DOMAIN 126 214 DISINTEGRIN-LIKE.
FT DOMAIN 215 359 CYS-RICH.
FT DOMAIN 360 416 EGF-LIKE.
FT DISULFID 31 115 BY SIMILARITY.
FT DISULFID 186 199 POTENTIAL.
FT DISULFID 360 375 BY SIMILARITY.
FT DISULFID 369 381 BY SIMILARITY.
FT DISULFID 383 392 BY SIMILARITY.
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 452 AA; 48577 MW; D11F66C24CDD6847 CRC64;

Query Match 59.5%; Score 375; DB 1; Length 452;
Best Local Similarity 58.3%; Pred. No. 9e-25;
Matches 63; Conservative 12; Mismatches 27; Indels 6; Gaps 2;

Qy 1 PTKLFEPECGNGVGEAGEGDCGCFHVC-----GLCKCKSLNSGAGSDGPCNNNTSC 56
Db 120 PLKLLDPSCGNGFVEAGEEBCDCGSGVOCSPRAGCKCKCTLTSHDAMCSDGLCCR--GC 177
Qy 57 LFQPRGYECRDVAVECDITEYCTGDSGQCPNHLKOGVACNONGRC 104

Db 178 KPEPRTVCRESLNECDVPEACPDSSACPAHLHKQDGYFCNDEQRC 225

RESULT 4

AD22_MOUSE STANDARD; PRT; 857 AA.
AC Q9R1V6; Q9R1V5; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22).
GN ADAM22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Brain;
RX MEDLINE=99365303; PubMed=10433968;
RA Sague K., Yamazaki K., Mizui Y., Tanaka I.;
RL "Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23",
Gene 236:79-86 (1999).
CC - FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - ALTERNATIVE PRODUCTS: Type I membrane protein.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q9R1V6-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q9R1V6-2; Sequence=VSP_005485;
CC - TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE BRAIN.
CC - PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC - SIMILARITY: Belongs to peptidase family M12B.
CC - SIMILARITY: Contains 1 EGF-like domain.
CC - SIMILARITY: Contains 1 disintegrin domain.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB009674; BAA83382.1; -
DR EMBL; AB009674; BAA83383.1; -
DR HSSP; P18619; 1FVL.
DR MEROPS; M12_978; -
DR MGD; MGI:1340046; Adam22.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Reptolysin.
DR InterPro; IPR006025; Zn_MTPptidse.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01421; Reptolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; D1SIN; 1.
DR PROSITE; PS50215; ADAM_MERPO; 1. FALSE_NEG.
DR PROSITE; PS50427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS50024; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
DR Signal; Glycoprotein; Transmembrane; EGF-like domain;
KW Alternative splicing.

FT SIGNAL 1 23
FT PROPEP 24 223
FT CHAIN 224 857
FT DOMAIN 24 734
FT TRANSMEM 735 755
FT DOMAIN 756 857
FT DOMAIN 224 436
FT DOMAIN 442 529
FT DOMAIN 533 666
FT DOMAIN 673 710
FT DISULFID 347 431
FT DISULFID 501 514
FT DISULFID 677 692
FT DISULFID 686 698
FT DISULFID 700 709
FT CARBOHYD 517 163
FT CARBOHYD 517 517
FT CARBOHYD 632 632
FT CARBOHYD 673 673
FT VARSPLIC 766 801
SQ SEQUENCE 857 AA; 94740 MW; CB88F87000208E09 CRC64;
Query Match 57.9%; Score 364.5; DB 1; Length 857;
Best Local Similarity 57.0%; Pred. No. 1.1e-23;
Matches 61; Conservative 14; Mismatches 27; Indels 5; Gaps 2;

QY 1 PTKLPEPCEGNGVYAEEDCCGPHVECT--GLCKCKSLSNAGHSDDPCNNITGCL 57
DB 436 PSKLLDPEPCGNGFETEEEDCCGPAECALGAECCCKCTLTQDSQSDGLCK--RCK 493
QY 58 FQPRGYECRDVNECDITEYCTGDSGCCPPNHLHKQDGYACNONGRC 104
DB 436 FQPLGTGVEAVNDCCDIEICSGNSQCAPVHKWDGISCCTGTCIC 540

RESULT 5

AD22_HUMAN STANDARD; PRT; 906 AA.
AC Q9P0K1; Q75075; Q75076; Q9P0K2; Q9U1A1; Q9UUK2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)
DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein
DE 2) (Metalloproteinase-disintegrin ADAM22-3).
GN ADAM22 OR MDC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=20504287; PubMed=11050470;
RA Harada T., Nishie A., Torigoe K., Ikezaki K., Shono T., Maehara Y.,
RA Kuwano M., Wada M.;
RT "The specific expression of three novel splice variant forms of human
RT metalloproteinase-like disintegrin-like cysteine-rich protein 2 gene
RT in brain tissues and gliomas".
RL Jpn. J. Cancer Res. 91:1001-1006 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RC TISSUE=Brain;
RX MEDLINE=98359734; PubMed=9693107;
RX Sague K., Ohya Y., Hasegawa Y., Tanaka I.;
RT "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2
RT and MDC3: novel human cellular disintegrins highly expressed in the
RL brain".
RL Biochem. J. 334:93-98 (1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 5).
RP TISSUE=Brain;
RC Wada M., Torigoe K., Harada T., Kuwano M.;

RT "Isolation and tissue specific expression of novel ADAM family from
 RT 7q21.1 region."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 40-906 FROM N.A. (ISOFORM 1).
 RC TISSUE=Cerebellum;
 RA MEDLINE=99453762; Pubmed=10524237;
 RA Poldinger K., Nelson N., Dubose R.F., Black R.A., Cerretti D.P.;
 RT "The identification of seven metalloproteinase-disintegrin (ADAM)
 RL Gene from genomic libraries."
 CC Gene 23761-70(1999).
 CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
 CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Dsilon;
 CC IsoId=09P0K1-1; Sequence=displayed;
 CC Name=2; Synonyms=Delta;
 CC IsoId=09P0K1-2; Sequence=VSP_005482; VSP_005484;
 CC Name=3; Synonyms=Alpha;
 CC IsoId=09P0K1-3; Sequence=VSP_005483;
 CC Name=4; Synonyms=Beta;
 CC IsoId=09P0K1-4; Sequence=VSP_005482; VSP_005483;
 CC Name=5;
 CC IsoId=09P0K1-5; Sequence=VSP_005482;
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE BRAIN. DETECTED SLIGHTLY
 CC OR NOT AT ALL IN OTHER TISSUES
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC or send an email to license@inb-ebi.ch).
 CC -----
 DR EMBL; AF155382; AAF73289.1; -
 DR EMBL; AF155381; AAF73288.1; -
 DR EMBL; AB009671; BAA32349.1; -
 DR EMBL; AB009671; BAA32350.1; -
 DR EMBL; AF073291; AAF22476.2; -
 DR EMBL; AF158637; AAD55251.1; -
 DR HSSP; P18619; 1FVL.
 DR MEROPS; M12.978; -
 DR GENES; HGNC:201; ADAM22.
 DR MIM; 603709; -
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0005178; F:integrin binding activity; NAS.
 DR GO; GO:0007162; P:negative regulation of cell adhesion; NAS.
 DR InterPro; IPR006586; ADAM cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR002870; Pep_M12B_propep.
 DR InterPro; IPR001590; Reptolysin.
 DR InterPro; IPR006025; Zn_MTpeptidse.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reptolysin; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR PRODOM; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS00425; ADAM_MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN; 1; FALSE_NEG.
 DR PROSITE; PS00214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.

DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 KW Signal; Glycoprotein; Transmembrane; EGF-like domain;
 KM Alternative splicing.
 FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 222 BY SIMILARITY.
 FT CHAIN 223 906 ADAM 22.
 FT DOMAIN 223 736 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 737 757 POTENTIAL.
 FT DOMAIN 758 906 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 223 438 METALLOPROTEASE-LIKE.
 FT DOMAIN 444 531 DISINTEGRIN-LIKE.
 FT DOMAIN 532 678 CYS-RICH.
 FT DOMAIN 675 712 EGF-LIKE.
 FT DISULFID 349 433 BY SIMILARITY.
 FT DISULFID 503 516 POTENTIAL.
 FT DISULFID 679 694 BY SIMILARITY.
 FT DISULFID 688 700 BY SIMILARITY.
 FT DISULFID 702 711 BY SIMILARITY.
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 768 803 Missing (in isoform 2, isoform 4 and
 FT isoform 5).
 FT VARSPPLIC 860 906 /FTId=VSP_005482.
 FT VARSPPLIC 859 859 Missing (in isoform 3 and isoform 4).
 FT VARSPPLIC 859 859 /FTId=VSP_005483.
 FT CONFLICT 81 81 E -> EYLNMPFRDINVAKVEDVANKTEPYFR (in
 FT isoform 2).
 FT SEQUENCE 906 AA; 100432 MW; 265ECDD0FA6C088B CRC64;
 SQ
 Query Match 57.7%; Score 363.5; DB 1; Length 906;
 Best Local Similarity 57.0%; Pred. No. 1,4e-23;
 Matches 61; Conservative 14; Mismatches 27; Indels 5; Gaps 2;
 QY 1 PTKLFEPTGECGVVEAGEGDCGFHVECY---GLCKKCSLSNGAHCSDGPCNNNTSCL 57
 Db 438 PSKLDPEECGNGFIETGECDCGTAEVLEGAECCKKTLVQDSGCSGLCK--KCK 495
 QY 58 FQPRGVECRDAVNECDITTEYCTGDSGQCPNHLKODGACNONGRC 104
 Db 496 FQPMGTGCREAVNVDCDIRTCGNSGSCAPNHHKMDGVCSDGVQIC 542
 RESULT 6
 AD22_XENLA STANDARD; PRT; 935 AA.
 ID AD22_XENLA
 AC 042596;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)
 DE (Metalloproteinase-disintegrin MDC11b) (MDC11.2).
 GN ADAM22 OR: MDC11B.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA MEDLINE=99102794; Pubmed=9882486;
 RA Cai H., Kraetzschmar J., Alfandari D., Hunnicutt G., Blobel C.P.;
 RT "Neural crest-specific and general expression of distinct
 RT metalloproteinase-disintegrins in early Xenopus laevis development."
 RL Dev. Biol. 204:508-524(1998).
 RN [2]
 RP SEQUENCE OF 464-511 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97349132; Pubmed=9205136;

RA Shilling F.M., Kraetzschmar J., Cai H., Weskamp G., Gayko U.,
 RA Lebow J., Myles D.G., Nucitelli R., Blobel C.P.;
 RT "Identification of metalloprotease/diintegrins in *Xenopus laevis*
 RT testis with a potential role in fertilization.",
 RU Biol. 166:155-164(1997).
 CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
 CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: LOW LEVELS IN ADULT TISSUES. NOT DETECTED IN
 CC DEVELOPING EMBRYOS.
 CC -1- PFM: THE PRECURSOR IS CLEAVED BY A PURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC -----
 CC EMBL, AF032383; AAC61847.1; -;
 CC EMBL, U78188; AAB87148.1; -;
 CC HSSP; P17347; 2ECH.
 CC
 CC MEROPS: M12_UBP; -;
 CC InterPro: IPR006586; ADAM cysteine.
 CC InterPro: IPR001762; Disintegrin.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR006210; IEGF.
 CC InterPro: IPR002870; Pep_M12B_propep.
 CC InterPro: IPR001590; Reprolysin.
 CC InterPro: IPR006025; Zn_MTPeptide.
 CC Pfam; PF00200; disintegrin; 1.
 CC Pfam; PF01562; Pep_M12B_propep; 1.
 CC Pfam; PF01421; Reprolysin; 1.
 CC ProDom; PD000664; Disintegrin; 1.
 CC SMART; SM00608; ACR; 1.
 CC SMART; SM00608; DISIN; 1.
 CC SMART; SM00181; EGF; 1.
 CC DR PROSITE; PS50215; ADAM_MEROP; 1.
 CC DR PROSITE; PS50427; DISINTEGRIN_1; 1.
 CC DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS01186; EGF_2; FALSE NEG.
 CC DR PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
 CC DR PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
 CC Signal; Glycoprotein; Transmembrane; EGF-like domain.
 CC SIGNAL 1 24
 CC FT PROPEP 25 227
 CC FT CHAIN 228 935
 CC FT DOMAIN 228 736
 CC FT TRANSMEM 727 757
 CC FT DOMAIN 728 935
 CC FT DOMAIN 228 440
 CC FT DOMAIN 446 533
 CC FT DOMAIN 536 670
 CC FT DOMAIN 677 713
 CC FT DISULFID 351 435
 CC FT DISULFID 505 518
 CC FT DISULFID 681 695
 CC FT DISULFID 689 701
 CC FT DISULFID 703 712
 CC FT CARBOHYD 167 167
 CC FT CARBOHYD 210 210
 CC FT CARBOHYD 521 521
 CC FT CARBOHYD 609 609
 CC FT CARBOHYD 636 636
 CC FT CARBOHYD 677 677
 CC SEQUENCE 935 AA, 104161 MW, 7787AEDCC5C77C90 CRC64;
 Query Match 56.7%; Score 357.5; DB 1; Length 935;

Best Local Similarity 57.0%; Pred. No. 4,66-23;
 Matches 61; Conservative 13; Mismatches 28; Indels 5; Gaps 2;
 Oy 1 PTKLPEPTCCNGVVEAGEEDCGFHWECY---GLCKKSGLSNGAHSDPCCNNISCL 57
 Db 440 PLKLLDPECCNGVVEAGEEDCGFHWECY---GLCKKSGLSNGAHSDPCCNNISCL 57
 Oy 58 FQPRGVECRDVAINECDITVEYCTGSDGCPPLHKKDGYACQNGQRC 104
 Db 498 FNPKEMLCREAVNCDIPETGTGNTSCCPANIHKLDDGSCSMQGLC 544
 RESULT 7
 AD33 HUMAN
 ID AD33 HUMAN STANDARD; PRT; 813 AA.
 AC O99B11;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM 33 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
 DE domain 33).
 GN ADAM33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Testis;
 RX MEDLINE=21674006; PubMed=11814695;
 RA Yoshinaka T., Nishii K., Yamada K., Sawada H., Nishiwaki E., Smith K.,
 RA Yoshino K., Ishiguro H., Higashiyama S.;
 RT "Identification and characterization of novel mouse and human ADAM33s
 RT with potential metalloprotease activity.";
 RL Gene 282:227-236(2002).
 RN [2]
 RP SEQUENCE OF 86-813 FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Buttrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cobby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaeashah M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycanore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9B211-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9B211-2; Sequence=VSP_005495;
 CC

CC -1- TISSUE SPECIFICITY: Expressed in all tissues, except: liver, with
 CC high expression in placenta, lung, spleen and veins.
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC or send an email to license@ebi.ac.uk).

DR EMBL: AB055891; BAB83092.1; -
 DR EMBL: AL356755; CAC16509.2; -
 DR HSSP: P18619; 1FVL.
 DR MEROPS: M12.239; -
 DR Genew: HGNC:15478; ADAM33.
 DR MIM: 607114; -
 DR GO: GO:0016021; C:integral to membrane; NAS.
 DR GO: GO:0004222; F:metalloendopeptidase activity; NAS.
 DR GO: GO:0008270; F:zinc ion binding activity; NAS.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR GO: GO:0042127; P:regulation of cell proliferation; ISS.
 DR GO: GO:0042035; P:regulation of cytokine biosynthesis; ISS.
 DR InterPro: IPR005686; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR001818; Matrxin.
 DR InterPro: IPR002870; Pep_M12B_propep.
 DR InterPro: IPR001590; Retriolysin.
 DR InterPro: IPR006025; Zn_MTPeptide.
 DR Pfam: PF00200; disintegrin_1.
 DR Pfam: PF01562; Pep_M12B_propep; 1.
 DR Pfam: PF01421; Retriolysin; 1.
 DR PRINTS: PR00289; DISINTEGRIN.
 DR ProDom: PD000664; disintegrin; 1.
 DR SMART: SM00608; ACR; 1.
 DR SMART: SM00500; DISIN; 1.
 DR PROSITE: PS50215; ADAM_MEPPO; 1.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 DR PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR Hydrolase: Metalloprotease; zinc; signal; glycoprotein; zymogen;
 KW Transmembrane; EGF-like domain; Alternate splicing.
 FT SIGNAL 1 29
 FT PROPEP 30 203
 FT CHAIN 204 813
 FT DOMAIN 30 701
 FT TRANSMEM 702 722
 FT DOMAIN 723 813
 FT DOMAIN 204 409
 FT DOMAIN 417 502
 FT DOMAIN 503 648
 FT DOMAIN 649 681
 FT SITE 133 133
 FT SITE 345 345
 FT METAL 346 346
 FT ACT_SITE 349 349
 FT METAL 355 355
 FT DISULFID 320 404
 FT DISULFID 360 388
 FT DISULFID 475 488
 FT DISULFID 653 663
 FT DISULFID 657 669
 FT DISULFID 671 680
 FT CARBOHYD 109 109

FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 636 661 Missing (in isoform 2).
 FT SEQUENCE 813 AA; 87738 MW; 90713A956805569 CRC64;
 SO
 Query Match 46.3%; Score 292; DB 1; Length 813;
 Best Local Similarity 51.0%; Pred. No. 1.2e-17;
 Matches 51; Conservative 11; Mismatches 34; Indels 4; Gaps 2;
 OY 7 PTEGNGYVADGEEDCGFHVECYGLCC--KCSLSGACMSDGPCCNNTSCLFQPGGYE 64
 DB 417 PALCGNFEVAGEECDCGPGCECRDLCCFAHNCSLRPGACCAHGDCC--VRCLIKPAGAL 474
 OY 65 CRDAVNECDITVECTSGSGCCPRLHKQDPAACNQGRC 104
 DB 475 CRQMGDCDLPEFCTGSSHCPDVYLLDGPSCARGSGYC 514
 RESULT 8
 ID AD15_RAT STANDARD; PRT: 816 AA.
 AC Q9QYV0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
 DE domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-
 DE rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
 DE (Mecarygadin) (CRII-7).
 GN ADAM15 OR MDC15.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sciatic nerve;
 RX MEDLINE=20556183; PubMed=11102971;
 RA Bosse F., Petzold G., Greiner-Petler R., Pipplars U., Gillen C.,
 RA Mueller H.-W.;
 RT "Cellular localization of the disintegrin CRII-7/MDC15 mRNA in rat
 RT PNS and CNS and regulated expression in postnatal development and
 RT after nerve injury";
 RL Glia 32:313-327(2000);
 CC -1- FUNCTION: May be involved in cell-surface proteolysis, cell
 CC adhesion or intracellular protein maturation.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (Potential).
 CC -1- SUBUNIT: Interacts with ITGA5-ITGB3 (vitronectin receptor),
 CC PACSIN3 and SNX. PACSIN3 and SNX9 preferentially bind the
 CC precursor but not the processed form of ADAM15, suggesting that
 CC the interaction occurs in a secretory pathway compartment prior to
 CC the medial Golgi (By similarity). Interacts specifically with Src
 CC family protein-tyrosine kinases (PTKs) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, SPINAL CORD,
 CC SCIATIC NERVE AND LUNG. EXPRESSED AT LOWER LEVELS IN ALL OTHER
 CC TISSUES. IN THE PERIPHERAL NERVOUS SYSTEM, EXPRESSED PREDOMINANTLY
 CC BY SCHWANN CELLS. IN THE CENTRAL NERVOUS SYSTEM, PREFERENTIALLY
 CC EXPRESSED BY NEURONAL CELLS.
 CC -1- INDUCTION: IN RESPONSE TO SCIATIC NERVE INJURY.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
 CC SORTING NEXIN 9 (BY SIMILARITY).
 CC -1- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA-V-BETA3 (BY
 CC SIMILARITY).
 CC -1- PTM: Phosphorylation increases association with PTKs (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC	-1- SIMILARITY: Contains 1 disintegrin domain.
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-stb.ch/announce/
CC	or send an email to license@isb-stb.ch).
CC	-----
DR	EMBL; AJ251198; CAB61762.1; -
DR	HSSP; P17494; 1KST.
DR	MEROPE; M12.215; -
DR	InterPro; IPR006586; ADAM_Cysteine.
DR	InterPro; IPR001762; Disintegrin.
DR	InterPro; IPR006209; EGF-like.
DR	InterPro; IPR001818; Matrxlin.
DR	InterPro; IPR002870; Pep_M12B_propep.
DR	InterPro; IPR001590; RepPolysitin.
DR	InterPro; IPR006025; Zn_MTpeptase.
DR	Pfam; PF00200; disintegrin; 1.
DR	Pfam; PF01562; Pep_M12B_propep; 1.
DR	Pfam; PF01421; RepPolysin; 1.
DR	ProDom; PD000664; disintegrin; 1.
DR	SMART; SMO0608; ACR_1.
DR	SMART; SMO0508; DISIN_1.
DR	PROSITE; PS50215; ADAM_MERO, 1. FALSE_NEG.
DR	PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR	PROSITE; PS50214; DISINTEGRIN_2; 1.
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.
DR	PROSITE; PS01186; EGF_2; 1.
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.
DR	PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
KW	Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
KW	Transmembrane; EGF-like domain; Sh3-binding; Phosphorylation.
FT	SIGNAL 1 17
FT	PROPEP 18 208 BY SIMILARITY.
FT	CHAIN 209 816 ADAM_15.
FT	DOMAIN 209 698 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 699 719 POTENTIAL.
FT	DOMAIN 720 816 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 209 416 METALLOPROTEASE.
FT	DOMAIN 423 510 DISINTEGRIN-LIKE.
FT	DOMAIN 511 658 CYS-RICH.
FT	DOMAIN 659 687 EGF-LIKE.
FT	DOMAIN 700 713 POLY-LEU.
FT	SITE 768 774 SH3-BINDING (POTENTIAL).
FT	SITE 803 809 SH3-BINDING (POTENTIAL).
FT	SITE 180 180 CYSTEINE SWITCH.
FT	SITE 350 350 ZINC (CATALYTIC) (POTENTIAL).
FT	ACT_SITE 351 351 POTENTIAL.
FT	METAL 354 354 ZINC (CATALYTIC) (POTENTIAL).
FT	METAL 360 360 ZINC (CATALYTIC) (POTENTIAL).
FT	DISULFID 325 411 BY SIMILARITY.
FT	DISULFID 482 495 POTENTIAL.
FT	DISULFID 659 669 BY SIMILARITY.
FT	DISULFID 663 675 BY SIMILARITY.
FT	DISULFID 677 686 BY SIMILARITY.
FT	MOD_RES 717 717 PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES 737 737 PHOSPHORYLATION (BY SIMILARITY).
FT	CARBOHYD 57 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD 239 239 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD 391 391 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD 394 394 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD 608 608 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD 613 613 N-LINKED (GLCNAC...) (POTENTIAL).
SO	SEQUENCE 816 AA; 88051 MW; B9D2CB023266FC27 CRC64;
Query Match	44.1%; Score 278; DB 1; Length 816;
Best Local Similarity	48.5%; Pred. No. 1,8e-16;
Matches 50; Conservative 12; Mismatches 31; Indels 10; Gaps 4	

Db 426 CGMVFVPGEGCCDGGFEDECTDPCCDYFTQGLRGAGACGABDPECCN--CKLPGAGNQR 483
Oy 67 DAVNECDITECTGDSGQCEPNNHKODGYACNQNQ-----GRC 104
Db 484 LPDPCDLPFCGLDSSQCPFDLTLGGEGPCASGEAVCMHGRC 526

RESULT 9
ADIS_HUMAN
ID ID15
AC AC13444; Q13493; O96C78;
DT DT16-OCT-2001 (Rel. 40, Created)
DT DT15-SEP-2003 (Rel. 42, Last sequence update)
DE DE ADAM15 precursor (BC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein) (Metargidin)
DE DE ADAM15 OR MDC15.
OS OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX OX NCBI_TaxID=9606;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RC RC TISSUE=Breast carcinoma;
RX RX MEDLINE=96214870; PubMed=8617717;
RA RA Kraitschmar J., Lum L., Blobel C.P.;
RT RT "Metargidin, a membrane-anchored metalloprotease-disintegrin protein with an RGD integrin binding sequence".
RL RL J. Biol. Chem. 271:4593-4596 (1996).
RN RN [2]
RP RP SEQUENCE FROM N.A.
RC RC TISSUE=umbilical vein;
RX RX MEDLINE=97192141; PubMed=9039960;
RA RA Herren B., Raines E.W., Ross R.;
RT RT "Expression of a disintegrin-like protein in cultured human vascular cells and in vivo".
RL RL FASEB J. 11:173-180(1997).
RN RN [3]
RP RP SEQUENCE FROM N.A.
RA RA Katkainen I., Huovila A.-P.J.;
RT RT "The characteristic structure of human ADAM15 gene structure and promoter region".
RL RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN RN [4]
RP RP SEQUENCE FROM N.A.
RC RC TISSUE=Kidney;
RX RX MEDLINE=22388257; PubMed=12477932;
RA RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Wuzny D.M., Sodeyren E.-J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Senech A., Schein J.E., Jones S.J.W., Maira M.A.;
RT RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
RN RN Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
RN RN [5]
RP RP INTERACTION WITH INTEGRIN ALPHA-V-BETA3.
RX RX MEDLINE=96184837; PubMed=9516430;

RA Zhang X.P., Kamata T., Yokoyama K., Puzon-McLaughlin W., Tekada Y.,
 RT "Specific interaction of the recombinant disintegrin-like domain of
 RT MDC-15 (metcargidin, ADAM-15) with integrin alphavbeta3.";
 RL J. Biol. Chem. 273:7345-7350 (1998).
 RN [6].
 RP PHOSPHORYLATION OF TYR-715 AND TYR-735.
 RX MEDLINE=21826475; PubMed=11741929;
 RA Pochovyan Z., Robbins S.M., Houslay M.D., Webster A., Murphy G.,
 RA Edwards D.R.;
 RT "Phosphorylation-dependent interactions between ADAM15 cytoplasmic
 RT domain and Src family protein-tyrosine kinases.";
 RL J. Biol. Chem. 277:4999-5007 (2002).
 CC -1- FUNCTION: May be involved in cell-surface proteolysis, cell
 CC adhesion or intracellular protein maturation.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBUNIT: Interacts with ITGA9-ITGB3 (Vitellogenin receptor),
 CC PACS3 and SNX9. PACS3 and SNX9 preferentially bind the
 CC precursor but not the processed form of ADAM15, suggesting that
 CC the interaction occurs in a secretory pathway compartment prior to
 CC the medial Golgi (By similarity). Interacts specifically with Src
 CC family protein-tyrosine kinases (PTKs).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. OVEREXPRESSED IN
 CC ARTERIOSCLEROTIC LESIONS. CONSTITUTIVELY EXPRESSED IN CULTURED
 CC ENDOTHELIAL AND SMOOTH MUSCLE.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
 CC SORTING NEXIN 9 (By similarity).
 CC -1- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHAHV-BETA3.
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- PTM: Phosphorylation increases association with PTKs.
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC -----
 DR EMBL; U46005; AACSI112.1; -;
 DR EMBL; U41767; AACSO404.1; -;
 DR EMBL; AF314227; AAM4189.1; -;
 DR EMBL; BC014566; AAM41566.1; -;
 DR HSSP; P18619; IFLV.
 DR MEROPS; M12.215; -;
 DR Genew; HGNC:193; ADAM15.
 DR MIM; 605548; -;
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
 DR InterPro; IPR006586; ADAM-cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001818; Matrxin.
 DR InterPro; IPR002870; Pep_M12B_propep.
 DR InterPro; IPR001590; Repolysin.
 DR InterPro; IPR006025; Zn_Mpeptidase.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Repolysin; 1.
 DR Prodom; PD000664; Disintegrin; 1.
 DR SMART; SM00608; ACR_1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS00215; ADAM_MEROP; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS00214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 DR Hydrolase; Metalloprotease; Zinc; signal; Glycoprotein; Zymogen;

KW Transmembrane; EGF-like domain; SH3-binding; Phosphorylation.
 FT SIGNAL 1 17
 FT PROPEP 18 206
 FT CHAIN 207 814
 FT DOMAIN 207 696
 FT TRANSMEM 697 717
 FT DOMAIN 718 814
 FT DOMAIN 207 414
 FT DOMAIN 421 508
 FT DOMAIN 509 656
 FT DOMAIN 657 685
 FT SITE 766 772
 FT SITE 801 807
 FT SITE 179 179
 FT SITE 484 486
 FT METAL 348 348
 FT ACT_SITE 349 349
 FT METAL 352 352
 FT METAL 358 358
 FT DISULFID 323 409
 FT DISULFID 480 493
 FT DISULFID 657 667
 FT DISULFID 661 673
 FT MOD_RES 715 715
 FT MOD_RES 735 735
 FT CARBOHYD 389 389
 FT CARBOHYD 392 392
 FT CARBOHYD 606 606
 FT CARBOHYD 611 611
 FT CONFLICT 714 714
 FT CONFLICT 791 791
 SQ SEQUENCE 814 AA; 87716 MW; 683A8368AD30996B CRC64;
 Query Match 43.5%; Score 274; DB 1; Length 814;
 Best Local Similarity 48.5%; Pred. No. 4e-16;
 Matches 50; Conservative 11; Mismatches 32; Indels 10; Gaps 4;
 Oy 10 CGNGYVAGEECDDGFHVECYGLCKK--GSLNGAIC-SIGPRCNCNTSCIFORGVYCR 66
 Db 424 CGNFFVEGEGCDDGFDDCDVPCDSLTCLRGACACASGPGCON--COLRPSGWCR 481
 Oy 67 DAVNECDITEYCTDSGCGCPNLHKDGYACNQNO-----GRC 104
 Db 482 PTRGDCDLPFCFSDSSCCPPDVSLGDEPCAGQAVCMGRG 524
 RESULT 10
 AD33 MOUSE STANDARD: PRT: 797 AA.
 AC Q923W9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM33 precursor (BC 3.4.24.-) (A disintegrin and
 DE metalloprotease domain 33).
 GN ADAM33.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=21674006; PubMed=11814695;
 RA Yoshinaka T., Nishii K., Yamada K., Sawada H., Nishiwaki E., Smith K.,
 RA Yoshino K., Ishiguro H., Higashiyama S.;
 RT "Identification and characterization of novel mouse and human ADAM33s
 RT with potential metalloprotease activity.";
 RL Gene 282:227-236 (2002).
 RN [2]
 RP SEQUENCE OF 113-797 FROM N.A. (ISOFORM 1).

CC STRAIN-Swiss Webster / NIH;
 RA Smith K.M., Alfandari D., White J.M., Sutherland A.E., Desimone D.W.;
 RT "M-ADAM3 cloned from mouse embryo day 11 cDNA library."
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBA databases.
 CC -1- COPACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q923W9-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q923W9-2; Sequence=VSP_005496;
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FORIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL, AB059633; BAB84337.1; -;
 CC EMBL, AB059632; BAB84336.1; -;
 CC EMBL, AF366072; AAK67164.1; -;
 CC MGD, MG1:141813; Adam33.
 CC GO, GO:0016021; C:Integral to membrane; NAS.
 CC GO, GO:0004222; F:metalloendopeptidase activity; NAS.
 CC GO, GO:0008270; F:zinc ion binding activity; NAS.
 CC GO, GO:0006508; P:proteolysis and peptidolysis; NAS.
 CC GO, GO:004127; P:regulation of cell proliferation; NAS.
 CC GO, GO:0042035; P:regulation of cytokine biosynthesis; NAS.
 CC InterPro: IPR006586; ADAM_cysteine.
 CC InterPro: IPR001762; Disintegrin.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR001818; Matrxin.
 CC InterPro: IPR002870; Pep_M12B_propep.
 CC InterPro: IPR001580; Repolysin.
 CC InterPro: IPR006025; Zn_MTPeptidse.
 CC Pfam, PF01562; Pep_M12B_propep; 1.
 CC Pfam, PF01421; Repolysin; 1.
 CC PRINTS: PR00289; DISINTEGRIN.
 CC ProDom, PD000664; Disintegrin; 1.
 CC SMART, SM00608; ACR, 1.
 CC SMART, SM00608; ACR, 1.
 CC PROSITE, PS00050; DISIN, 1.
 CC PROSITE, PS0215; ADAM_MPRO, 1.
 CC PROSITE, PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 CC PROSITE, PS00427; DISINTEGRIN_1; FALSE_NEG.
 CC PROSITE, PS0214; DISINTEGRIN_2; 1.
 CC PROSITE, PS00022; EGF_1; FALSE_NEG.
 CC PROSITE, PS01186; EGF_2; 1.
 CC PROSITE, PS00142; ZINC_PROTEASE; 1.
 CC HydroLase: Metalloprotease; Zinc; Signal: Glycoprotein; Zymogen;
 KW Transmembrane; EGF-like domain; Alternative splicing.
 FT SIGNAL 1 29
 FT PROPEP 1 29
 FT CHAIN 1 29
 FT DOMAIN 205 797
 FT TRANSMEM 703 723
 FT DOMAIN 724 797
 FT DOMAIN 205 797
 FT DOMAIN 418 503
 FT DOMAIN 504 649
 FT DOMAIN 650 682
 FT DOMAIN 767 772
 FT SITE 134 134
 FT METAL 346
 FT ACT_SITE 347

FT METAL 350 350 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 356 356 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 321 405 BY SIMILARITY.
 FT DISULFID 351 389 BY SIMILARITY.
 FT DISULFID 476 489 POTENTIAL.
 FT DISULFID 654 664 BY SIMILARITY.
 FT DISULFID 658 670 BY SIMILARITY.
 FT DISULFID 672 681 BY SIMILARITY.
 FT VARSPLIC 637 662 Missing (in isoform 2).
 FT FT 319 326 GICRAESS -> DMREGLSF (IN REF. 2).
 FT CONFLICT 725 725 MISSING (IN REF. 2).
 FT SEQUENCE 797 AA; 86954 MW; E405FC1B852C65FF CRC64;
 SQ
 Query Match 42.7%; Score 269; DB 1; Length 797;
 Best Local Similarity 45.3%; Pred. No. 1e-15; Indels 4; Gaps 2;
 Matches 48; Conservative 14; Mismatches 40;
 QY 1 PTKLPEPTCGNGVYAGREDCGFHVCYGLCC--KKCSLSNGAHCSGRCNNTSCLF 58
 DB 412 PGLVLPRCGNGFLEAGEBCDCGSGQKCPDPCFPHNCSLRAGNCAHGDCC--ARCLL 469
 QY 59 QPRGECRDVAVNEDITYCTGDSGQCPNHLKQDGYACNONGRC 104
 DB 470 KSAQPCRPATDCLPFCFTGTSPYCPADVYLLDSDPCABGRGYC 515

Search completed: October 21, 2003, 10:06:24
 Udo time : 19.3145 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:53:36 ; Search time 72.6038 Seconds
(without alignments)
369.643 Million cell updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630
Sequence: 1 PTLFEPTECGNGYVAGEE.....CPNLHKQDGYAKNORQGRG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	832	4	075077
2	611	97.0	690	11	08CC33
3	611	97.0	829	11	09R1V7
4	292	46.3	812	4	08N0W6
5	283	44.9	617	13	090499
6	276.5	43.9	587	5	08R319
7	276.5	43.9	959	5	09VPH0
8	275	43.7	451	13	09PT49
9	274	43.5	797	11	08R465
10	269	42.7	797	11	08R465
11	269	42.7	790	4	08R827
12	267.5	42.5	790	4	08R827
13	263	41.7	609	13	08B0N1
14	263	41.7	809	11	08C882
15	263	41.7	864	11	08C720
16	259.5	41.2	1023	5	0967H9

17	259	41.1	914	13	012960	012960 xenopus lae
18	258	41.0	610	13	09Y120	09Y120 agkistrodon
19	258	41.0	836	6	019057	019057 pongo pygma
20	255	40.5	609	13	090282	090282 crocatus at
21	255	40.5	620	13	042138	042138 agkistrodon
22	254	40.3	212	13	090Y44	090Y44 agkistrodon
23	254	40.3	609	13	09W6M5	09W6M5 agkistrodon
24	254	40.3	610	13	093523	093523 bothrops ja
25	254	40.3	610	13	08Q688	08Q688 bothrops in
26	252.5	40.1	600	13	09PVK7	09PVK7 naja naja
27	251	39.8	612	13	08UVG0	08UVG0 bothrops er
28	251	39.8	804	11	060410	060410 cavia porce
29	249	39.5	180	13	093518	093518 agkistrodon
30	249	39.5	899	13	08UVF1	08UVF1 coturnix co
31	247.5	39.3	655	4	08NFM6	08NFM6 homo sapien
32	247	39.2	761	11	08CDV3	08CDV3 mus musculu
33	246.5	39.1	845	11	061072	061072 mus musculu
34	246	39.0	614	13	08J1R1	08J1R1 timaresuru
35	245.5	39.0	702	11	08BWR5	08BWR5 mus musculu
36	245.5	39.0	714	11	08K4K0	08K4K0 mus musculu
37	245.5	39.0	873	13	042595	042595 xenopus lae
38	245	38.9	604	13	09PT48	09PT48 atractaspis
39	244.5	38.8	610	13	08AW15	08AW15 agkistrodon
40	244.5	38.8	612	13	090213	090213 timaresuru
41	244	38.7	606	13	098UP9	098UP9 bothrops ja
42	244	38.7	694	5	09GZ15	09GZ15 drosophila
43	244	38.7	791	11	060813	060813 mus musculu
44	244	38.7	1182	5	09VXLI	09VXLI drosophila
45	243	38.6	216	13	09PSN7	09PSN7 crocatus ru

ALIGNMENTS

RESULT 1
ID 075077 PRELIMINARY; PRT; 832 AA.
AC 075077;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MDC3 (ADAM22 protein).
OS ADAM22.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=98359734; PubMed=9693107;
RA Sagan K., Ohya Y., Hasegawa Y., Tanaka I.,
RT "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2
RT and MDC3: novel human cellular disintegrins highly expressed in the
RT brain.";
RT Biochem. J. 334:93-98(1998).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC Cal S., Lopez-Otin C.,
RT "Identification and characterization of ADAM 22, a novel
RT metalloproteinase/disintegrin protein.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB009672; BAA32351.1; -;
DR EMBL; AJ005580; CAC20565.1; -;
DR HSSP; P18619; IFVL.
DR MEROPS; M12.979; -;
DR Genew; HGNC:202; ADAM23.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002870; Pep_M12B_propep.

DR InterPro; IPR001590; Reprolysin.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Peg_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SO SEQUENCE 832 AA; 91935 MW; 7841A9670E1C24EF CRC64;

Query Match 100.0%; Score 630; DB 4; Length 832;
Best Local Similarity 100.0%; Pred. No. 1.9e-67;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PTKLFEPTCEGNGVYAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFQP 60
DB 496 PTKLFEPTCEGNGVYAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFQP 555
61 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 104
556 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 599

RESULT 2
ID 08CC33 PRELIMINARY; PRT; 690 AA.
AC 08CC33.
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE A disintegrin and metalloprotease domain 23.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dienccephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT Nature 420:563-573(2002)."
RL Nature 420:563-573(2002).
DR EMBL; AK034022; BAC28550.1; -
SO SEQUENCE 690 AA; 77228 MW; B6169914AEC6A6 CRC64;

Query Match 97.0%; Score 611; DB 11; Length 690;
Best Local Similarity 96.2%; Pred. No. 3e-65;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PTKLFEPTCEGNGVYAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFQP 60
DB 493 PTKLFEPTCEGNGVYAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFQS 552
61 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 104
553 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 596

RESULT 3
ID 09R1V7 PRELIMINARY; PRT; 829 AA.
AC 09R1V7.
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE ADAM23.
GN ADAM23.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99365303; PubMed=10433968;
RA Sagane K., Yamazaki K., Mizui Y., Tanaka I.;
RT "Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23."
RL Gene 236:79-86(1999)
DR EMBL; AB009673; BAA83381.1; -
DR HSSP; P18619; IEVL.
DR MEROPS; M12.979; -
DR MGP; MGI:1345162; ADAM23.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR00162; Disintegrin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002870; Peg_M12B_propep.
DR InterPro; IPR001590; Reprolysin.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Peg_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SO SEQUENCE 829 AA; 91547 MW; FE6BCD69DD50F53A CRC64;

Query Match 97.0%; Score 611; DB 11; Length 829;
Best Local Similarity 96.2%; Pred. No. 3.6e-65;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PTKLFEPTCEGNGVYAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFQP 60
DB 493 PTKLFEPTCEGNGVYAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFQS 552
61 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 104
553 RGYECRDVAVNECDITEYCTGDSGQCPNHLKODGYACNONGRC 596

RESULT 4
ID 08N0W6 PRELIMINARY; PRT; 812 AA.
AC 08N0W6.
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE A disintegrin and metalloprotease domain 33.
GN ADAM33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RX MEDLINE=22116089; PubMed=12110844;
RA Van Eerdewegh P., Little R.D., Dupuis J., Del Mastro R.G., Falls K.,
RA Simon J., Torrey D., Pandit S., McKenny J., Braunschweiger K.,
RA Walsh A., Liu Z., Hayward B., Folz C., Manning S.P., Bawa A.,
RA Saracino L., Thackston M., Benchekroun Y., Capparelli N., Wang M.,
RA Adair R., Feng Y., Dubois J., Fitzgerald M.G., Huang H., Gibson R.,
RA Allen K.M., Pedan A., Danzig M.R., Umland S.P., Egan R.W., Cuss F.M.,
RA Roke S., Clough J.B., Holloway J.W., Holgate S.T., Keith T.P.;
RT "Association of the ADAM33 gene with asthma and bronchial
RT hypersponsiveness.";
RL Nature 418:426-430(2002).
DR EMBL; AF466287; AAM80482.1; -

DR EMBL, AF466288; AAM80483.1; -
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR002870; pep_M12B_propep.
 DR InterPro: IPR001590; Reptolysin.
 DR InterPro: IPR006025; Zn_MTPeptide.
 DR Pfam: PF00200; disintegrin_1.
 DR Pfam: PF01562; pep_M12B_propep; 1.
 DR Pfam: PF01421; Reptolysin; 1.
 DR PRINTS: PR00289; DISINTEGRIN.
 DR ProDom: PD000664; disintegrin; 1.
 DR SMART: SM00608; ACR; 1.
 DR SMART: SM00050; DISIN; 1.
 DR PROSITE: PS50215; ADAM_MERO; 1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR Integrin; Metalloprotease; Protease.
 KW SEQUENCE 812 AA; 87667 MW; EBA817363E2489EC CRC64;

Query Match 46.3%; Score 292; DB 4; Length 612;
 Best Local Similarity 51.0%; Pred. No. 1.1e-26;
 Matches 51; Conservative 11; Mismatches 34; Indels 4; Gaps 2;

QY 7 PTECGNGVYAGEECDCGFHVECYGLCC--KKCSLSNGAHCSDPCCNNTSCLFQPRGYE 64
 DB 417 PALCNGFVEAGEECDCGPGEGCRDLCCFHNCSLRFAGQCAHDDCC--VRCLKAPGAL 474
 QY 65 CRDAVNECDITTEYTCGSGCCPNNLHKODGYACNONGRC 104
 DB 475 CROMAGDCDLPEFCTGTSNHPDVYLLDGSPCARGSGYC 514

RESULT 5

ID Q90499 PRELIMINARY; PRT; 617 AA.
 AC Q90499;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Metalloprotease.
 GN ECHI.
 OS Echis pyramidum (carpet viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;
 OC Viperidae; Viperinae; Echis.
 NC NCB1_TaxID=8700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=85010025; PubMed=7925363;
 RA Paine M.J.I., Moura-Da-Silva A.M., Theakston R.D.G., Crempson J.M.;
 RT "Cloning of metalloprotease genes in the carpet viper (Echis pyramidum
 RT laekeyi). Further members of the metalloprotease/disintegrin gene
 RT family";
 RL Eur. J. Biochem. 224:483-488(1994).
 DR EMBL: J78970; CA55565.1; -
 DR HSSP: P18619; 1FVL.
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR002870; pep_M12B_propep.
 DR InterPro: IPR001590; Reptolysin.
 DR InterPro: IPR006025; Zn_MTPeptide.
 DR Pfam: PF00200; disintegrin; 1.
 DR Pfam: PF01562; pep_M12B_propep; 1.
 DR Pfam: PF01421; Reptolysin; 1.
 DR PRINTS: PR00289; DISINTEGRIN.
 DR ProDom: PD000664; disintegrin; 1.
 DR SMART: SM00608; ACR; 1.
 DR SMART: SM00050; DISIN; 1.
 DR PROSITE: PS50215; ADAM_MERO; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00427; DISINTEGRIN_1; 1.

DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Protease.
 FT CHAIN 193 617 METALLOPROTEASE.
 SO SEQUENCE 617 AA; 69310 MW; 83DCDAS4F3AFA CRC64;

Query Match 44.9%; Score 283; DB 13; Length 617;
 Best Local Similarity 44.8%; Pred. No. 9.8e-26;
 Matches 47; Conservative 17; Mismatches 37; Indels 4; Gaps 2;

QY 2 TKLPEPTCGNGVYAGEECDCGFHVECYGLCC--KCSLSNGAHCSDPCCNNTSCLFQ 59
 DB 399 TDIVSPSCGNVYFVEAGEECDCSRTYCRNPPCNATTKLTPGSCADGECCN--QCRFR 456
 QY 60 PRGYECRDVNECDITTEYTCGSGCCPNNLHKODGYACNONGRC 104
 DB 457 PARTCCRKIDCDVPEYCTGSGCEPLDVFRNGQPYQSNNGYC 501

RESULT 6

ID Q8T319 PRELIMINARY; PRT; 587 AA.
 AC Q8T319;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE S003917D.
 GN CG31314 OR CG7649.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY095096; AAM11424.1; -
 DR FLYBase: FBgn0051314; CG31314.
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001590; Reptolysin.
 DR InterPro: IPR006025; Zn_MTPeptide.
 DR Pfam: PF00200; disintegrin; 1.
 DR Pfam: PF01421; Reptolysin; 1.
 DR ProDom: PD000664; Disintegrin; 1.
 DR SMART: SM00608; ACR; 1.
 DR SMART: SM00050; DISIN; 1.
 DR PROSITE: PS50215; ADAM_MERO; 1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 SO SEQUENCE 587 AA; 63507 MW; 3D910ADF283365DB CRC64;

Query Match 43.9%; Score 276.5; DB 5; Length 587;
 Best Local Similarity 45.8%; Pred. No. 5.7e-25;
 Matches 49; Conservative 16; Mismatches 39; Indels 3; Gaps 2;

QY 1 PTKLPEPTCGNGVYAGEECDCGFHVECYGLCC--KKCSLSNGAHCSDPCCNNTSCL 57
 DB 76 PERLFESPTCGNFGVEAGEECDCGPRHCNACNQTCLMLHKNATCATGECDDLTTCR 135
 QY 58 FQPRGYECRDVNECDITTEYTCGSGCCPNNLHKODGYACNONGRC 104
 DB 136 PKLAGSACREAVNECDLPEYCTGSEYCPADVFRFRDTEPCDGGQAYC 182

RESULT 7
 Q9VFH0 PRELIMINARY; PRT: 959 AA.
 ID Q9VFH0
 AC Q9VFH0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2000 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG31314 protein.
 GN CG31314 OR CG7649.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydrioidae; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Branton R.C., Rogers Y.H.C., Blazey R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt C., Nelson C.R., Miklos G.L.G.,
 RA Abill J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Duran-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Mishina N.V., Modyaty C., Morris J., Moshireli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sienkiewicz I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strung R., Sun E.,
 RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster";
 Science 287:2185-2195 (2000).
 [2]
 RP SEQUENCE FROM N.A.
 RP Celinker S.E., Adams M.D., Krommiller B., Man K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Branton R.C., Rogers Y.,
 RA Banton J., An H., Baldwin D., Banton J., Beeson K.Y., Busam D.A.,
 RA Carlson J., Center A., Champagne M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dossert V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Fries E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshireli A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Peltman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svitzkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 "Sequencing of Drosophila melanogaster genome";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Miya S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
 RA Klomp W., Drysdale R., Emmert D., Fries E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of Drosophila melanogaster genome";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003705; AAF55088.2; -.
 DR HSSP; P18619; 1FVL.
 DR Flybase; FBgn0051314; CG31314.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR002870; Pcp_M12B.
 DR InterPro; IPR001590; Reprolysin.
 DR InterPro; IPR006025; Zn_MTPepidase.
 DR Pfam; PF00200; disintegrin_1.
 DR Pfam; PF01562; Pcp_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPPO; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 959 AA; 105329 MW; E60F9309F4ACE3C6 CRC64;
 Query Match 43.9%; Score 276.5; DB 5; Length 959;
 Best Local Similarity 45.8%; Pred. No. 9.3e-25;
 Matches 49; Conservative 16; Mismatches 39; Indels 3; Gaps 2;
 QY 1 PTKLPEPFCNGVYAGEECDCGFHYECYGLCC--KKCSL-SNGAHCSDPCCNNTSCL 57
 DB 448 PERLPFESTCGNGFVPEPQDCDGLPEHCENACCAQTCMLHSHKATCATGECDDTTCR 507
 QY 58 FQPRGVECDRAVNECDITETCTGDSGQCPNVLHKQDGYACNQNQGR 104
 DB 508 PKLAGSACREANEDCDLPEYCTGSESEYCPADVFRDTEPCDGGQAYC 554
 RESULT 8
 Q9PT49 PRELIMINARY; PRT: 451 AA.
 ID Q9PT49
 AC Q9PT49
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Metalloproteinase precursor (Fragment).
 OS Atractaspis engadensis (Israeli burrowing asp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scieroglossa; Serpentes; Colubroidae;
 OC Atractaspididae; Atractaspidis.
 NCBI_TaxID=8600;
 [1]
 RP SEQUENCE FROM N.A.
 RP Tissue=venom gland;
 RC Tissue=venom gland;
 RA Duencel F.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF186368; AAF01040.1; -.
 DR HSSP; P18619; 1FVL.

DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR001590; Reprolysin.
 DR InterPro: IPR006025; Zn_MTPepdse.
 DR Pfam: PF00200; disintegrin; 1.
 DR Pfam: PF01421; Reprolysin; 1.
 DR ProDom: PD000664; Disintegrin; 1.
 DR SMART: SM00608; ACR; 1.
 DR SMART: SM00505; DISIN; 1.
 DR PROSITE: PS50215; ADAM_MEPPO; 1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 2
 FT CHAIN 31 235
 FT CHAIN 236 328
 FT SEQUENCE 451 AA; 50286 MW; 8C1395BF9B9D3EF8 CRC64;
 Query Match 43.7%; Score 275; DB 13; Length 451;
 Best Local Similarity 48.0%; Pred. No. 6.6e-25;
 Matches 48; Conservative 11; Mismatches 37; Indels 4; Gaps 2;
 QY 7 PTEGNGVYGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLFOPRGYE 64
 DB 243 PAVGNGVFEVGEBCDGGSPQECQACCNATTCQLQHGACDSEGCDD--CQRLKGAGAE 300
 QY 65 CRDAVNECDITEYCTGDSGCGCPNHLKODGYACNONGRC 104
 DB 301 CRAMDECDPELCTGDSABECTTDLQRNGOPCENNQGFC 340
 RESULT 9
 ID 096C78 PRELIMINARY; PRT; 814 AA.
 AC 096C78.
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE A disintegrin and metalloproteinase domain 15 (metacridin)
 DE (Metalloprotease disintegrin).
 GN ADAM15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strauberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Karkkainen I., Huovila A.-P.J.;
 RT "The characterization of human ADAM15 gene structure and promoter
 RT region."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014566; AAH4566.1; -
 DR EMBL: AF314227; AAM4189.1; -
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR002870; Pep_M12B_propep.
 DR InterPro: IPR001590; Reprolysin.
 DR InterPro: IPR006025; Zn_MTPepdse.
 DR Pfam: PF00200; disintegrin; 1.
 DR Pfam: PF01562; Pep_M12B_propep; 1.
 DR Pfam: PF01421; Reprolysin; 1.
 DR ProDom: PD000664; Disintegrin; 1.
 DR PROSITE: PS50215; ADAM_MEPPO; 1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR Signal.
 KW Integrin; Protease.

SO SEQUENCE 814 AA; 87717 MW; 683AB368AD30996B CRC64;
 Query Match 43.5%; Score 274; DB 4; Length 814;
 Best Local Similarity 48.5%; Pred. No. 1.6e-24;
 Matches 50; Conservative 11; Mismatches 32; Indels 10; Gaps 4;
 QY 10 CGNGVYAGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLFOPRGYECR 66
 DB 424 CGNMFVEVGEBCDGFDDCVDPCCDSLTCQLRPGACASDGPCCQN--CQLRPSGQCR 481
 QY 67 DAVNECDITEYCTGDSGCGCPNHLKODGYACNONGRC 104
 DB 482 PTRDDCDLPEFCPPDSSQCPDVSLGDEPCAGGQAVCMHGRG 524
 RESULT 10
 ID 08R465 PRELIMINARY; PRT; 797 AA.
 AC 08R465.
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE ADAM33.
 GN ADAM33.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/HeJ;
 RA Gunn T.M., Azarani A., Kim P., Hyman R.W., Davis R.W., Barsh G.S.;
 RT "Identification and preliminary characterization of mouse Adam33."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY054984; AAL14350.1; -
 DR MGD: MGI:1341813; Adam33.
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR002870; Pep_M12B_propep.
 DR InterPro: IPR001590; Reprolysin.
 DR InterPro: IPR006025; Zn_MTPepdse.
 DR Pfam: PF00200; disintegrin; 1.
 DR Pfam: PF01562; Pep_M12B_propep; 1.
 DR Pfam: PF01421; Reprolysin; 1.
 DR ProDom: PD000664; Disintegrin; 1.
 DR SMART: SM00608; ACR; 1.
 DR SMART: SM00505; DISIN; 1.
 DR PROSITE: PS50215; ADAM_MEPPO; 1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 SO SEQUENCE 797 AA; 87009 MW; CB05B5FFD87E3E CRC64;
 Query Match 42.7%; Score 269; DB 11; Length 797;
 Best Local Similarity 45.3%; Pred. No. 6.2e-24;
 Matches 48; Conservative 14; Mismatches 40; Indels 4; Gaps 2;
 QY 1 PTKLPEPTGNGVYAGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLF 58
 DB 412 PGLVLVPSRCNGVLEAGEBCDGGSCGCPFPANHCISLRAGACAHGDC--ARCLL 469
 QY 59 QPRVGECDVNECDITEYCTGDSGCGCPNHLKODGYACNONGRC 104
 DB 470 KSAQTPCRPAATDCDLPEFTGTSPYCPADVLLDGSPCAERGRG 515

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